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887535 PLANT?/BI 611283 PLANT?/AB 467117 STRESS?/BI 407910 STRESS?/AB 1063335 SELECT?/BI 958649 SELECT?/AB 887054 GENE#/BI 675169 GENE#/AB
L1 592 (PLANT? AND STRESS? AND SELECT? AND GENE#)/BI,AB

=> s l1 and regulat?/bi,ab 808933 REGULAT?/BI 593409 REGULAT?/AB
L2 205 L1 AND REGULAT?/BI,AB

=> s l2 not 2004/py 148190 2004/PY
L3 200 L2 NOT 2004/PY

=> s l3 not 2003/py 1101086 2003/PY
L4 161 L3 NOT 2003/PY

=> s l4 not 2002/py 1120422 2002/PY
L5 117 L4 NOT 2002/PY

=> s l5 not 2001/py 1075582 2001/PY
L6 96 L5 NOT 2001/PY

=> s l6 not 2000/py 1014602 2000/PY

L7 85 L6 NOT 2000/PY

=> d l7 1-85 bib ab

L7 ANSWER 1 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:812151 CAPLUS
DN 132:304069
TI A heat shock transcription factor in pea is differentially controlled by heat and virus replication
AU Aranda, Miguel A.; Escaler, Margarita; Thomas, Carole L.; Maule, Andrew J.
CS John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, UK
SO Plant Journal (1999), 20(2), 153-161 CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Science Ltd.
DT Journal
LA English
AB Since some heat-inducible ***genes*** [heat shock (hs) ***genes***] can be induced by virus infection in pea we have investigated the effect that heat and virus replication may have on the expression of a heat-shock transcription factor ***gene*** (Hsf). We have characterized what appears

to be the only member of the Hsf family in pea, PsHsfA. Similar to Hsp70, PsHsfA is heat-inducible in vegetative and embryonic tissues, which is concordant with the presence of heat shock elements (HSEs) and ***stress*** responsive elements (STREs) on its promoter sequence. The expression of PsHsfA during virus replication was studied in pea cotyledons and leaves, and compared to that of Hsp70. In situ hybridization expts. showed that whereas Hsp70 is induced, there is no detectable increased accumulation of PsHsfA RNA assocd. with the replication of pea seed-borne mosaic potyvirus (PSbMV). These expts. indicate that there is a ***selective*** control of virus-induced hs ***gene*** expression, and suggest that different ***regulatory*** pathways control hs ***gene*** expression during heat shock and virus replication.
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:436353 CAPLUS
DN 132:47594
TI Translational control in ***plant*** ***stress*** : the formation of messenger ribonucleoprotein particles (mRNPs) in response to desiccation of Tortula ruralis gametophytes
AU Wood, Andrew J.; Oliver, Melvin J.
CS Plant Stress and Water Conservation Unit, Lubbock, TX, 79401, USA
SO Plant Journal (1999), 18(4), 359-370 CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Science Ltd.
DT Journal
LA English
AB Changes in ***gene*** expression obsd. in vivo in response to desiccation and rehydration of the desiccation-tolerant bryophyte Tortula ruralis are ***regulated*** by alterations in the pattern of ***selection*** of mRNAs, from a qual. const. mRNA pool, by the translational machinery. When drying rates are slow, messenger ribonucleoprotein particles (mRNPs) are formed in the drying gametophytes. A representative rehydrin mRNA, Tr288, was sequestered into these particles which were analyzed using sucrose and CsCl gradients. Quant. RT-PCR anal. of the fractions from a low salt extn. demonstrated that Tr288 mRNA migrated farther in the sucrose gradient, relative to those extractable in high salt, indicating that the transcript is assocd. with particles that are of higher d. RT-PCR anal. also demonstrated that the majority of Tr288 mRNA, from slowly desiccated gametophytes, is assocd. with particles that have buoyant densities between 1.44 and 1.64 g cm-3 which correspond to the buoyant d. range reported for mRNP particles. MRNPs that are unique to drying T. ruralis gametophytes form at least four size classes after in vivo UV crosslinking based upon FPLC anal. This is the first report of mRNP formation in response to a vegetative water deficit in ***plants*** .
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:419413 CAPLUS
DN 131:155762
TI ***Plant*** biotechnology of flavonoids
AU Madhuri, G.; Reddy, Arjula R.
CS Sch. Life Sci., Univ. Hyderabad, 500046, India
SO Plant Biotechnology (Tokyo) (1999), 16(3), 179-199
CODEN: PLBIF6; ISSN: 1342-4580
PB Japanese Society for Plant Cell and Molecular Biology
DT Journal; General Review
LA English
AB A review with many refs. Flavonoids, including anthocyanins are ubiquitous compds. constituting about 5-10% of the known secondary metabolites imparting vivid floral, seed and foliage colors in ***plants*** ranging from bryophytes to angiosperms. ***Plants*** are specialized in synthesizing and accumulating specific combinations of flavonoids out of a pool of about 5000 known flavonoids implying their adaptive functions. The flavonoid pathway has been well characterized in a few ***select*** ***plants*** . The genetic and mol. anal. revealed that the pathway is governed by a no. of loci dispersed across the ***plant*** genome and ***regulated*** by distinct ***regulatory*** ***gene*** families in a temporal and spatial manner. With the rapid growth in mol. and biochem. characterization of the ***genes*** and their products it has now become possible to precisely elucidate the role of flavonoids in ***plant*** survival. Flavonoids have been implicated in diverse functions such as UV-B protection, signal mols. in ***plant*** -microbe symbiotic assocns., ***plant*** defense response, cold ***stress*** response, modulators of hormone response and pollen fertility. In addn., the role of flavonoids as very powerful dietary anti-oxidant supplements in human nutrition is increasingly demonstrated. The review highlights certain structural and functional aspects of flavonoids particularly their role in ***stress*** response. Further, recent advances in application of biotechnol. tools to manipulate flavonoid pathway in different ***plants*** has been described. Flavonoid ***genes*** as benign and visible reporters of ***plant*** origin in transformation expts. appears to be promising. Studies on transgenic ***plants*** carrying genetically engineered flavonoid ***genes*** leading to the accumulation of flavonoids by sense over-expression or decrease or elimination by anti-sense suppression resp., have been used to manipulate ***plants*** defense response against bacterial and fungal diseases. Flavonoid biotechnol. has become a powerful tool to manipulate flower color in horticulture industry. This review critically evaluates various functions of flavonoids and describes specific instances and strategies of biotechnol. manipulation to improve ***plant*** performance and value addn.

L7 ANSWER 4 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:385525 CAPLUS
DN 131:165943
TI Antisense-mediated depletion of potato leaf .omega.3 fatty acid desaturase lowers linolenic acid content and reduces ***gene*** activation in response to wounding
AU Martin, Marta; Leon, Jose; Dammann, Christian; Albar, Juan-Pablo; Griffiths, Gareth; Sanchez-Serrano, Jose J.
CS Plant Molecular Genetics, Centro Nacional de Biotecnologia CSIC, Madrid, 28049, Spain
SO European Journal of Biochemistry (1999), 262(2), 283-290
CODEN: EJBCAI; ISSN: 0014-2956
PB Blackwell Science Ltd.
DT Journal
LA English
AB Fatty acid .omega.3 desaturases act on membrane lipids to catalyze the formation of trienoic fatty acids, the most abundant in ***plant*** tissues being .alpha.-linolenic acid. This fatty acid is a precursor of jasmonic acid, a ***plant*** growth ***regulator*** involved in the control of wound-induced ***gene*** activation in ***plants*** and in the induction of tuberization in potato. We isolated a potato .omega.3 desaturase cDNA, possibly encoding a plastidial

isoform, and used it to investigate its expression pattern throughout ***plant*** development and in response to wounding. Plastidial .omega.3 desaturase ***gene*** transcripts accumulate rapidly upon wounding, preceding the jasmonate-dependent induction of the wound-responsive proteinase inhibitor II ***gene*** . We generated transgenic potato ***plants*** constitutively expressing an antisense RNA to this plastidial .omega.3 desaturase. ***Selected*** transgenic lines in which the cognate .omega.3 desaturase mRNA is largely depleted show a marked redn., of up to 60%, in trienoic acids in leaves and tubers. In these lines, a corresponding redn. in jasmonate content and proteinase inhibitor II expression is obsd. upon wounding. Our results indicate that a redn. in .omega.3 desaturase mRNA levels compromises the wound-induced activation of proteinase inhibitor II, suggesting that wound-induced synthesis of linolenic acid is required for jasmonic acid prodn. The antisense-mediated depletion of fatty acid .omega.3 desaturases is a viable alternative for reducing trienoic fatty acid content in ***plant*** species in which a mutant screening approach is not applicable.
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 5 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:223963 CAPLUS
DN 131:2756
TI Proline synthesis and degradation: a model system for elucidating ***stress*** -related signal transduction
AU Hare, P. D.; Cress, W. A.; Van Staden, J.
CS Natal University Research Unit for Plant Growth and Development, Department of Botany, University of Natal Pietermaritzburg, Scottsville, 3209, S. Afr.
SO Journal of Experimental Botany (1999), 50(333), 413-434 CODEN: JEBOA6; ISSN: 0022-0957
PB Oxford University Press
DT Journal; General Review
LA English
AB A review with 77 refs. A causal relationship between increased proline synthesis and ***plant*** tolerance of hyperosmotic ***stresses*** has been demonstrated. Nonetheless, the mol. basis of this effect is not yet established. Proline accumulation appears to be mediated by both ABA-dependent and ABA-independent signalling pathways, although the events that occur between the perception of ***stress*** and the induction of proline biosynthetic ***genes*** are poorly characterized. Recent evidence supports an important role for post-transcriptional events in dehydration- and ABA-induced proline synthesis. Further research concerning the factors that ***regulate*** the expression of enzymes involved in proline synthesis and degrdn. will not only be of value in attempts to increase ***plant*** ***stress*** tolerance, but may contribute to an improved understanding of at least certain ***stress*** -related aspects of the ***regulatory*** network which controls ***plant*** responses to the environment. In Arabidopsis thaliana, synthesis of the immediate precursor of proline, .DELTA.1-pyrroline-5- carboxylate (P5C), is apparently ***regulated*** by a pathway disrupted by mutation of ABI1, a protein serine/threonine phosphatase of the 2C class. Similarities and differences between the signalling events upstream of the ***regulation*** of the ***gene*** encoding P5C synthetase and model ***stress*** -inducible Arabidopsis ***genes*** such as RD29A, KIN2, and RAB18 are reviewed. Further anal. of the factors that induce these ***genes*** may assist in elucidating the mechanisms involved in ***stress*** -induced proline accumulation. Putative ***stress*** - ***regulated*** promoter elements in the AtP5CS1, AtP5CS2 and AtP5CR ***genes*** are identified. Recent evidence that a signal related to proline synthesis and/or degrdn. ***selectively*** increases the expression of ***stress*** -related ***genes*** underscores the importance of elucidating the signalling events assocd. with proline accumulation under adverse conditions.
RE.CNT 77 THERE ARE 77 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 6 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:150709 CAPLUS
DN 130:279359
TI Mutations affecting induction of glycolytic and fermentative ***genes*** during germination and environmental ***stresses*** in Arabidopsis
AU Conley, Terry R.; Peng, Hsiao-Ping; Shih, Ming-Che
CS Department of Biological Sciences, University of Iowa, Iowa City, IA, 52242, USA
SO Plant Physiology (1999), 119(2), 599-607 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
AB Expression of the alc. dehydrogenase ***gene*** (ADH) of Arabidopsis is known to be induced by environmental ***stresses*** and ***regulated*** developmentally. The authors used a neg.- ***selection*** approach to isolate mutants that were defective in ***regulating*** the expression of the ADH ***gene*** during seed germination; they then characterized three recessive mutants, aar1-1, aar1-2, and aar2-1, which belong to two complementation groups. In addn. to their defects during seed germination, mutations in the AAR1 and AAR2 ***genes*** also affected anoxic and hypoxic induction of ADH and other glycolytic ***genes*** in mature ***plants*** . The aar1 and aar2 mutants were also defective in responding to cold and osmotic ***stress*** . The two allelic mutants aar1-1 and aar1-2 exhibited different phenotypes under cold and osmotic ***stresses*** . Apparently, these mutants are defective in a late step of the signaling pathways that lead to increased expression of the ADH ***gene*** and glycolytic ***genes*** .
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 7 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:46731 CAPLUS
DN 130:247480
TI New molecular approaches to improving salt tolerance in crop ***plants***
AU Winicov, I.
CS Departments of Microbiology and Biochemistry, University of Nevada Reno, Reno, NV, 89557, USA
SO Annals of Botany (London) (1998), 82(6), 703-710 CODEN: ANBOA4; ISSN: 0305-7364
PB Academic Press
DT Journal; General Review
LA English
AB A review with 75 refs. The last century has seen enormous gains in ***plant*** productivity and in resistance to a variety of pests and diseases through much innovative ***plant*** breeding and more recently mol. engineering to prevent ***plant*** damage by insects. In contrast, improvements to

salt and drought tolerance in crop and ornamental ***plants*** has been elusive, partially because they are quant. traits and part of the multigenic responses detectable under salt/drought ***stress*** conditions. However, the rapidly expanding base of information on mol. strategies in ***plant*** adaptation to ***stress*** is likely to improve exptl. strategies to achieve improved tolerance. Recently studies of salinity tolerance in crop ***plants*** have ranged from genetic mapping to mol. characterization of salt/drought induced ***gene*** products. With our increasing understanding of biochem. pathways and mechanisms that participate in ***plant*** ***stress*** responses it has also become apparent that many of these responses are common protective mechanisms that can be activated by salt, drought and cold, albeit sometimes through different signalling pathways. This review focuses on recent progress in mol. engineering to improve salt tolerance in ***plants*** in context of our current knowledge of metabolic changes elicited by salt/drought ***stress*** and the known ***plant*** characteristics useful for salt tolerance. While it is instructive to draw parallels between mol. mechanisms responsive to salt- ***stress*** with accumulating evidence from studies of related abiotic ***stress*** -responses, more data are needed to delineate those mechanisms specific for salt tolerance. Also discussed is the alternative genetic strategy that combines single-step ***selection*** of salt tolerant cells in culture, followed by regeneration of salt tolerant ***plants*** and identification of ***genes*** important in the acquired salt tolerance. Currently, transgenic ***plants*** have been used to test the effect of overexpression of specific prokaryotic or ***plant*** ***genes*** , known to be up- ***regulated*** by salt/drought ***stress*** . The incremental success of these expts. indicates a potentially useful role for these ***stress*** -induced ***genes*** in achieving long term tolerance. In addn., it is possible that enhanced expression of ***gene*** products that function in physiol. systems esp. sensitive to disruption by salt, could incrementally improve salt tolerance. Current knowledge points towards a need to reconcile our findings that many ***genes*** are induced by ***stress*** with the practical limitations of overexpressing all of them in a ***plant*** in a tissue specific manner that would maintain developmental control as needed. New approaches are being developed towards being able to manipulate expression of functionally related classes of ***genes*** by characterization of signalling pathways in salt/drought ***stress*** and characterization and cloning of transcription factors that ***regulate*** the expression of many ***genes*** that could contribute to salt/drought tolerance. Transcription factors that ***regulate*** functionally related ***genes*** could be particularly attractive targets for such investigations, since they may also function in ***regulating*** quant. traits. Transgenic manipulation of such transcription factors should help us understand more about multigene ***regulation*** and its relationship to tolerance. (c) 1998 Annals of Botany Company.
RE.CNT 75 THERE ARE 75 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 8 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:44491 CAPLUS
DN 130:219069
TI Alfin1, a novel zinc-finger protein in alfalfa roots that binds to promoter elements in the salt-inducible MsPRP2 ***gene***
AU Bastola, Dhundy R.; Pethe, Vaijaynti V.; Winicov, Ilga
CS Departments of Microbiology and Biochemistry School of Medicine, University of Nevada Reno, Reno, NV, 89557, USA
SO Plant Molecular Biology (1998), 38(6), 1123-1135 CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer Academic Publishers
DT Journal
LA English
AB Alfin1 cDNA, obtained by differential screening of a poly(A)+ library from salt-tolerant alfalfa cells, encodes a novel protein with a Cys4 and His/Cys3 putative zinc-binding domain that suggests a possible role for this protein in transcriptional ***regulation*** . We have expressed the cDNA in Escherichia coli and show that the recombinant Alfin1 protein binds DNA in a sequence-specific manner. The DNA recognition sequence was detd. from individual clones isolated after four rounds of random oligonucleotide ***selection*** in gel retardation assays, coupled with PCR amplification of the ***selected*** sequences. The consensus binding site for Alfin1 is shown to contain two to five G-rich triplets with the conserved core of GNGGTG or GTGGNG in clones showing high-efficiency binding. DNA binding of the recombinant Alfin1 was inhibited by EDTA. Alfin1 mRNA was found predominantly in alfalfa roots. Growth of salt-sensitive Medicago sativa L on 171 mM NaCl led to a slight decrease in Alfin1 mRNA, while the salt-tolerant ***plants*** showed no decrease in Alfin1 mRNA levels. Interestingly, recombinant Alfin1 binds efficiently to three fragments of the MsPRP2 promoter, each contg. consensus sequences identified by the random oligonucleotide ***selection*** . Since MsPRP2 transcripts were shown to be root-specific and accumulated in alfalfa roots in a salt-inducible manner, Alfin1 may play a role in the ***regulated*** expression of MsPRP2 in alfalfa roots and contribute to salt tolerance in these ***plants*** .
RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 9 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:113 CAPLUS
DN 130:165523
TI Differential ***regulation*** of enolase during anaerobiosis in maize
AU Lal, Shailesh K.; Lee, Chwenfang; Sachs, Martin M.
CS Department of Crop Sciences, University of Illinois at Urbana-Champaign, Urbana, IL, 61801, USA
SO Plant Physiology (1998), 118(4), 1285-1293 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
AB It was reported previously that enolase enzyme activity and ENO1 transcript levels are induced by anaerobic ***stress*** in maize (Zea mays). Here we show that not all isoforms of maize enolase are anaerobically induced. We cloned and sequenced a second enolase cDNA clone (pENO2) from maize. Sequence anal. showed that pENO2 shares 75.6% nucleotide and 89.5% deduced amino acid sequence identity with pENO1 and is encoded by a distinct ***gene*** . Expression of ENO2 is constitutive under aerobic conditions, whereas ENO1 levels are induced 10-fold in maize roots after 24 h of anaerobic treatment. Western-blot anal. and N-terminal sequencing of in vivo-labeled maize roots identified two major proteins ***selectively*** synthesized upon anaerobic ***stress*** as isoenzymes of enolase. We describe the expression of enolase in maize roots under anaerobic ***stress*** .

RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 10 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:774023 CAPLUS
DN 130:76948
TI The identification of sugarcane ***genes*** by random sequencing of cDNA clones
AU Carson, D. L.; Huckett, B. I.; Botha, F. C.
CS SASA Experiment Station, Mount Edgecombe, 4300, S. Afr.
SO Proceedings of the Annual Congress - South African Sugar Technologists' Association (1998), 72nd, 143-145 CODEN: PSATAA; ISSN: 0373-045X
PB South African Sugar Technologists' Association
DT Journal
LA English
AB The aim of this study is to identify sugarcane ***genes*** expressed in the leaf roll and the mature stem. Random DNA sequencing of cDNA clones allows the identification of ***genes*** and the development of Expressed Sequence Tags (ESTs). A total of 250 clones randomly ***selected*** from a leaf roll cDNA library and 112 from a mature stem library have been sequenced. Homol. searches with sequences located in international databases have indicated a broad diversity of ***genes*** encoding proteins such as metabolic enzymes, structural proteins and ***regulatory*** factors. Preliminary analyses have indicated that although ***genes*** common to both the leaf roll and mature stem have been detected, several ***stress*** -related ***genes*** have been identified in the mature stem. Further studies will det. whether ESTs may be used to identify differentially expressed ***genes*** in sugarcane tissues.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 11 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:746751 CAPLUS
DN 130:134544
TI Biochemical events in the activation and attenuation of the heat shock transcriptional response
AU Satyal, Sanjeev H.; Morimoto, Richard I.
CS Department of Biochemistry, Molecular Biology and Cell Biology, Rice Institute for Biomedical Research, Northwestern University, Evanston, IL, 60208, USA
SO Journal of Biosciences (Bangalore, India) (1998), 23(4), 303-311 CODEN: JOBSDN; ISSN: 0250-5991
PB Indian Academy of Sciences
DT Journal; General Review
LA English
AB A review with 78 refs. The expression of heat shock proteins in response to cellular ***stress*** is mediated by a family of heat shock transcription factors (HSFs). The transcriptional activity of these HSFs is ***regulated*** by multiple redundant ***regulatory*** mechanisms which ensure the fine tuned expression of heat shock ***genes*** . These mechanisms include cis- ***regulatory*** domains and trans-acting proteins which modulate HSF activity and control the heat shock response. Heat shock ***gene*** expression is also ***regulated*** by ***selective*** use of various HSFs under distinct developmental and growth conditions.
RE.CNT 78 THERE ARE 78 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 12 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:714116 CAPLUS
DN 130:92813
TI Transcriptional and post-transcriptional processes ***regulate*** ***gene*** expression in oxygen-deprived roots of maize
AU Fennoy, Sheila L.; Nong, Thoa; Bailey-Serres, Julia
CS Department of Botany and Plant Sciences, University of California, Riverside, CA, 92521 0124, USA
SO Plant Journal (1998), 15(6), 727-735 CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Science Ltd.
DT Journal
LA English
AB To investigate the ***regulation*** of ***gene*** expression in maize (Zea mays L.) in response to oxygen deprivation (flooding), the authors quantitated run-on transcription in isolated nuclei, steady-state mRNA accumulation and mRNA loading with ribosomes for seven ***genes*** that encode proteins synthesized predominantly in oxygen-deprived roots (anaerobic polypeptides) and seven ***genes*** that encode proteins synthesized in aerobic roots (aerobic polypeptides). Run-on transcription of anaerobic polypeptide ***genes*** was induced in response to oxygen deprivation and run-on transcription of the aerobic polypeptide ***genes*** continued during the ***stress*** treatment. The increased accumulation of mRNAs that encode anaerobic polypeptides occurred concomitant with the induction of ***gene*** transcription and efficient assocn. of these mRNAs with large polysomes. The steady-state accumulation of aerobic polypeptide mRNAs was within twofold of aerobic levels and in a no. of cases fewer ribosomes were loaded per transcript. These results demonstrate that ***selected*** synthesis of anaerobic polypeptides involves transcriptional as well as significant post-transcriptional ***regulation*** of ***gene*** expression. The repression of synthesis of many aerobic polypeptides occurs without interruption of ***gene*** transcription and is due to translational ***regulation*** and possibly the sequestration of mRNAs on mRNPs. Ribosome loading patterns indicated that this translational control occurs at both initiation and post-initiation phases in a message-specific manner.
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 13 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:672675 CAPLUS
DN 129:271496
TI Viral vectors for identification of RNA ***regulatory*** sequences and interacting molecules
IN Blau, Helen M.; Spicher, Albert; Guicherit, Oivin
PA The Board of Trustees of the Leland Stanford Junior University, USA
SO PCT Int. Appl., 64 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 9842854 A1 19981001 WO 1998-US6093 19980327 W: CA, JP RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
PRAI US 1997-42543P P 19970327
AB Methods and compns. for the identification, characterization and isolation of ***regulatory*** RNA sequences are provided. ***Regulatory*** RNA sequences mediate post-transcriptional ***regulation*** in response to various environmental conditions and can be used to alter the

level of expression of endogenous ***genes*** or to identify factors which interact with ***regulatory*** RNA sequences. The invention addnl. provides improved vector systems for rapid screening, anal., and tightly- ***regulated*** expression of ***regulatory*** RNA sequences. The ***regulatory*** properties of highly conserved regions (HCRs) within 3'-UTRs that have retained greater than 70% homol. within stretches of 100 nucleotides over 30 million years were examd. A retroviral vector system was used with a ***selectable*** marker that allowed rapid delivery of 3'-UTR-reporter constructs to populations of thousands of cells within one to two weeks, avoiding problems assocd. with clonal anal. and long-term ***selection*** . Addnl., this vector is modular, thereby permitting direct comparison of different HCRs on ***gene*** expression, independent of 5'-UTRs, promoters, protein coding regions and polyadenylation signals. Ten HCRs (from c-fos, c-myc, transferrin receptor, bcl2, EF1.alpha., vimentin, ornithine decarboxylase, fibronectin, HuD and Ran ***genes***) were examd. Nine of these HCRs (i.e., all except the Ran HCR) were found to decrease mRNA stability to different extents. Two HCRs (the c-fos and vimentin HCRs) altered mRNA translation under steady-state conditions. Four HCRs (the HuD, Ran, fibronectin and ornithine decarboxylase HCRs) mediated responses to changes in mitogen level by increasing reporter protein levels 2-fold while 2 HCRs exhibited a 6-fold difference in their response to another environmental ***stress*** , hypoxia.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 14 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:672079 CAPLUS
DN 130:11246
TI Auxin-induced ***stress*** potentiates trans-activation by a conserved ***plant*** basic/leucine-zipper factor
AU Pascuzzi, Pete; Hamilton, David; Bodily, Kimbra; Arias, Jonathan
CS Center for Agricultural Biotechnology, University of Maryland, College Park, MD, 20742, USA
SO Journal of Biological Chemistry (1998), 273(41), 26631-26637 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB The promoter element activation sequence-1 (as-1) confers tissue-specific and signal-responsive transcription in ***plants*** . Hormone and chem. ***stress*** cues are thought to activate as-1-dependent transcription through specific basic/leucine-zipper proteins, termed TGA factors, that bind this element. The authors report here that a highly conserved TGA factor of tobacco, TGA1a, can ***selectively*** activate transcription in response to micromolar concns. of auxin hormones or their analogs. This induction is chem. specific, as a range of other compds. tested at similar concns. had little or no effect. Auxin was found to augment the trans-activation potential of TGA1a through carboxyl-terminal residues. The amino-terminal domain of TGA1a, by gain-of-function assays, was found to both constitutively activate transcription and maximize the response to auxin. Further evidence indicates that the trans-activation potential of this domain in TGA1a is repressed, under basal conditions, by carboxyl-terminal residues. Because TGA1a and endogenous TGA factors are stimulated by auxin only at concns. that inhibited cell growth, this response is likely to involve chem. ***stress*** .
RE.CNT 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 15 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:453128 CAPLUS
DN 129:161009
TI Iron, sulfur, and chlorophyll deficiencies: a need for an integrative approach in ***plant*** physiology
AU Imsande, John
CS Plant Genetics Group, Dept of Agronomy, Iowa State Univ., Ames, IA, 50011, USA
SO Physiologia Plantarum (1998), 103(1), 139-144 CODEN: PHPLAI; ISSN: 0031-9317
PB Munksgaard International Publishers Ltd.
DT Journal; General Review
LA English
AB A review with many refs. Green ***plants*** deficient in nitrogen, sulfur, or iron develop a similar yellow coloration. In each case, the yellow coloration is accompanied by a lowered chlorophyll concn. This review attempts to collate some of the biochem. information concerning these three seemingly diverse nutritive deficiencies and bares a need for a more integrative approach to ***plant*** physiol. The biochem. and biol. roles of nitrogen, sulfur and iron in living systems are examd., with emphasis on sulfur and iron. Mechanistically, iron and/or sulfur are highly reactive components of many enzymes. Indeed, iron and sulfur sometimes form Fe2S2, Fe3S4, or Fe4S4 clusters which are very active electron transfer agents. Recently, iron-sulfur clusters have been reported to serve as sensors of oxidative ***stress*** , to couple photosynthesis with several metabolic pathways, to participate in the redn. of sulfite and nitrite, and to participate in ***regulation*** of ***gene*** expression. Thus, there are several mechanisms by which a deficiency of nitrogen, sulfur, or iron could produce the same low-chlorophyll, yellow phenotype in ***plants*** . Unless the interactions and coordination of the various pathways connected to chlorophyll synthesis are elucidated, it is unlikely that we will ***select*** the quickest and most direct path to ***plant*** improvement.
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 16 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:425050 CAPLUS
DN 129:171251
TI CPRF4a, a novel ***plant*** bZIP protein of the CPRF family: comparative analyses of light-dependent expression, post-transcriptional ***regulation*** , nuclear import and heterodimerization
AU Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
CS Inst. Biologie II, Univ. Freiburg, Freiburg, D-79104, Germany
SO Molecular & General Genetics (1998), 257(6), 595-605 CODEN: MGGEAE; ISSN: 0026-8925
PB Springer-Verlag
DT Journal
LA English
AB Several DNA-binding proteins with conserved basic region/leucine zipper domains (bZIP) have been isolated from parsley. They all recognize defined ACGT- contg. elements (ACEs), including ACEPcCHSII in the Light ***Regulatory*** Unit LRU1 of the CHS promoter which confers light responsiveness. A new member of this Common ***Plant***

Regulatory Factor (CPRF) family, designated CPRF4a, has been cloned, which displays sequence similarity to HBP-1a from wheat, as well as to other ***plant*** bZIP proteins. CPRF4a specifically binds as a homodimer to ACEPcCHSII and forms heterodimers with CPRF1 but not with CPRF2. In adult parsley ***plants*** , CPRF2 and CPRF4a mRNAs are found in all tissues and organs in which the chalcone synthase ***gene*** CHS is expressed. In protoplasts from suspension cultured cells, UV irradn. (290-350 nm) did not cause an increase in levels of CPRF1, CPRF2, or CPRF4a mRNA, whereas the corresponding CPRF proteins accumulated within 15 min of light treatment. Furthermore, the rapid light-mediated increase of CPRF proteins was insensitive to transcriptional inhibitors, suggesting that a post-transcriptional mechanism controls CPRF accumulation. CPRFs as well as Arabidopsis thaliana G-box binding factors (GBFs) are ***selectively*** transported from the cytosol into the nucleus, as shown in an in vitro nuclear transport system prepd. from vacuolated parsley protoplasts, indicating that cytosolic compds. are involved in ***regulated*** nuclear targeting of ***plant*** bZIP factors.
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 17 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:400056 CAPLUS
DN 129:171223
TI Analysis of expressed ***genes*** in ethylene-treated potato leaves using expressed sequence tags
AU Kwon, Tae Ho; Yang, Moon Sik
CS Institute for Molecular Biology and Genetics, Chonbuk National University, Jeonju, 560-756, S. Korea
SO Journal of Plant Biology (1998), 41(1), 24-30 CODEN: JPBIEZ
PB Botanical Society of Korea
DT Journal
LA English
AB To isolate useful and interesting ***plant*** ***genes*** in large quantities, random sequencing of cDNA clones from potato leaf library treated with ethylene was performed. Partial sequences of randomly ***selected*** 210 clones with the insert of longer than 500 base pair (bp) as well as poly (A) tail have been compared with sequences in GenBank, EMBL and DDBJ nucleic acid databases and fostered 193 expressed sequence tags (ESTs). The 210 cDNA clones identified are related to various aspect of metabolic pathways such as glycolysis, amino acid synthesis, translation mechanism, ribosome synthesis, hormone response, ***stress*** response, ***regulation*** of ***gene*** expression, and signal transduction. Among the 193 ESTs, 12 ESTs (29 cDNA clones) appeared more than once and 181 ESTs appeared once regarded as a solitary group. Out of 210 clones, 29 clones (13.8%) have no similarity to the known nucleotide sequences and could serve as a potentially useful resource for ***plant*** mol. biol. referring to particular ***genes*** . Nucleotide sequencing to generate more ESTs from ethylene-induced as well as non-induced potato leaf is in progress as well.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 18 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:339434 CAPLUS
DN 129:91235
TI Characterization and expression of a heptaubiquitin ***gene*** from tomato
AU Rollfinke, Ingrid K.; Silber, Martina V.; Pfitzner, Ursula M.
CS Botanisches Institut, Ludwig-Maximilians Universitat, Munchen, D-80638, Germany
SO Gene (1998), 211(2), 267-276 CODEN: GENED6; ISSN: 0378-1119
PB Elsevier Science B.V.
DT Journal
LA English
AB Ubiquitin is highly conserved 76 amino acid protein involved, among other functions, in the ***selective*** degrdn. of proteins in the cell. From a tomato (Lycopersicon esculentum Mill. cv. Craigella) genomic library, the authors have isolated a clone encoding a polyubiquitin ***gene*** , designated ubq1-1 comprising seven repeats of ubiquitin and two C-terminal extension amino acids. The ubq1-1 ***gene*** contains an intron of 1128 bp immediately upstream of the translation start codon. DNA sequence comparison revealed that the 5' and 3' non-coding regions of the tomato ubq1-1 ***gene*** are nearly identical to the sequence of a polyubiquitin cDNA clone isolated from potato (Garbarino et al., 1992; ***Plant*** Mol. Biol. 20, 235-244). The ubq1-1 ***gene*** is expressed in leaves to rather low levels in tomato, and the abundance of ubq1-1 transcripts is increased under heat shock conditions. For functional analyses, a chimeric ***gene*** construct contg. the intron and 1.6 kb of ubq1-1 sequences 5' to the intron fused to the gus reporter ***gene*** was introduced into the tobacco genome. In leaves of transgenic tobacco ***plants*** , reporter ***gene*** expression was generally lower from the ubq1-1 promoter than from the cauliflower mosaic virus 35RNA promoter. In addn., the tomato ubq1-1 promoter was not found to respond to heat shock in transgenic tobacco ***plants*** . Histochem. anal. of the ***plants*** demonstrated localization of gus reporter ***gene*** activity in the vascular systems of the leaves and the roots. Deletion of the intron from the reporter ***gene*** construct markedly reduced reporter ***gene*** expression in transformed tobacco ***plants*** , thus suggesting that the intron may influence transcript levels deriving from the ubq1-1 promoter.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 19 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:254573 CAPLUS
DN 129:50143
TI Molecular markers and their use in QTL analysis
AU Quarrie, Steve; Lazic-Jancic, Vesna
CS John Innes Cent., Norwich Res. Park, Norwich, NR4 4UH, UK
SO Genetika (Zemun, Yugoslavia) (1996), (Suppl. 4), 15-27 CODEN: GNTKDF; ISSN: 0534-0012
PB Unija Bioloskih Naucnih Drustava Jugoslavije
DT Journal; General Review
LA English
AB A review with 45 refs. The advent of mol. markers (particularly RFLP- and PCR-derived) for use as probes for genomic DNA has revolutionized the genetic anal. of crop ***plants*** and provided not only geneticists, but also physiologists, agronomists and breeders with valuable new tools to identify traits of importance in improving resistance to abiotic ***stresses*** . For the breeder, a genetic map satd. with mol. markers allows ***selection*** for certain characters to be carried out much more efficiently and

effectively than was possible previously. High d. mol. maps allow the location of all major ***genes*** ***regulating*** the expression of a particular trait to be detd. Statistical methods have been developed to allow QTL for the trait to be identified. Not only does this allow the complexity of the genetic control of any trait to be detd., but by comparing the extent to which confidence intervals of QTL for different traits overlap it is possible to examine the likelihood that traits are pleiotropically linked. Thus, the traits most likely to be important in detg. yield under droughted conditions can be identified. Examples are given of mol. markers currently available and of their use to locate QTL for drought response traits in cereals.
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 20 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:233165 CAPLUS
DN 128:292695
TI Salt tolerance in crop ***plants*** : new approaches through tissue culture and ***gene*** ***regulation***
AU Winicov, Ilga; Bastola, Dhundy R.
CS Departments of Microbiology and Biochemistry, University of Nevada Reno, Reno, NV, 89557, USA
SO Acta Physiologiae Plantarum (1997), 19(4), 435-449
CODEN: APPLDE; ISSN: 0137-5881
PB Polish Academy of Sciences
DT Journal; General Review
LA English
AB A review and discussion with .apprx.100 refs. Recent approaches to study of salinity tolerance in crop ***plants*** have ranged from genetic mapping to mol. characterization of ***gene*** products induced by salt/drought ***stress*** . Transgenic ***plant*** design has allowed the effects of overexpression of specific prokaryotic or ***plant*** ***genes*** that are known to be up- ***regulated*** by salt/drought ***stress*** to be tested. This review summarizes current progress in the field in the context of adaptive metabolic and physiol. responses to salt ***stress*** and their potential role in long-term tolerance. Specifically considered are ***gene*** activation by salt, in view of proposed avenues for improved salt tolerance and the need to ascertain the addnl. influences of developmental ***regulation*** of such ***genes*** . Discussion includes the alternate genetic strategy that the authors have pursued for improving salinity tolerance in alfalfa (Medicago sativa L.) and rice (Oryza sativa L.). This strategy combines single-step ***selection*** of salt-tolerant cells in culture, followed by regeneration of salt-tolerant ***plants*** and identification of ***genes*** important in conferring salt tolerance. It was postulated that activation or improved expression of a subset of ***genes*** encoding functions that are particularly vulnerable under conditions of salt- ***stress*** could counteract the mol. effects of such ***stress*** and could provide incremental improvements in tolerance. The authors have proceeded to identify the acquired specific changes in ***gene*** ***regulation*** for salt-tolerant mutant cells and ***plants*** . One particularly interesting and novel ***gene*** isolate from the salt-tolerant cells is Alfin1, which encodes a putative zinc-finger ***regulatory*** protein, expressed predominantly in roots. This protein binds DNA in a sequence-specific manner and may be potentially important in ***gene*** ***regulation*** in roots in response to salt and an important marker for salt tolerance in crop ***plants*** .
RE.CNT 101 THERE ARE 101 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 21 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:158595 CAPLUS
DN 128:279487
TI Low temperature-stimulated phosphorylation ***regulates*** the binding of nuclear factors to the promoter of Wcs120, a cold-specific ***gene*** in wheat
AU Vazquez-Tello, A.; Ouellet, F.; Sarhan, F.
CS Departement Sciences biologiques, Universite Quebec Montreal, Montreal, QC, H3C 3P8, Can.
SO Molecular & General Genetics (1998), 257(2), 157-166
CODEN: MGGEAE; ISSN: 0026-8925
PB Springer-Verlag
DT Journal
LA English
AB The Wcs120 ***gene*** encodes a highly abundant protein which appears to play an important role during cold acclimation of wheat. To understand the ***regulatory*** mechanism controlling its expression at low temp., the promoter region has been characterized. Electrophoretic mobility shift assays using short promoter fragments revealed the presence in nuclear exts. from non-acclimated (NA) ***plants*** of multiple DNA-binding proteins which interact with several elements. In contrast, no DNA-binding activity was obsd. in the nuclear exts. from cold-acclimated (CA) ***plants*** . In vitro dephosphorylation of these CA nuclear exts. with alk. phosphatase restored the binding activity. Moreover, okadaic acid (a potent phosphatase inhibitor) markedly stimulated the in vivo accumulation of the WCS120 family of proteins. This suggests that protein phosphatases PP1 and/or PP2A neg. ***regulate*** the expression of the Wcs120 ***gene*** . In addn., both Ca2+-dependent and Ca2+-independent kinase activities were found to be significantly higher in the Ca nuclear exts. Western anal. using antibodies directed against protein kinase C (PKC) isoforms showed that a PKC.gamma. homolog (84 kDa) is ***selectively*** translocated into the nucleus in response to low temp. Taken together, our results suggest that, in vivo, the expression of the Wcs120 ***gene*** may be ***regulated*** by nuclear factors whose binding activity is modulated by a phosphorylation/dephosphorylation mechanism.
RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 22 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:88431 CAPLUS
DN 128:165068
TI Molecular tools for isolation and characterization of drought responsive ***genes*** in cereals
AU Gulli, Mariolina; Maestri, Elena; Malatrasi, Marina; Marmiroli, N.
CS Laboratory of Environmental Biotechnologies, Department of Environmental Sciences, University of Parma, Pharma, Italy
SO Drought and Plant Production, Proceedings [International Symposium], Lepenski Vir, Yugoslavia, Sept. 1996 (1997), Meeting Date 1996, Volume 2, 61-70. Editor(s): Jevtic, Stojan; Pekic, Sofija. Publisher: Agricultural Research Institute "Serbia", Belgrade, Yugoslavia. CODEN: 65OHAW
DT Conference
LA English
AB Drought ***stress*** is one of the most common and important abiotic ***stresses*** for ***plants*** . They can

be subjected to redn. in water availability in particular developmental conditions or as a consequence of environmental ***stresses*** . ***Plants*** can activate mechanisms at physiol., biochem. and mol. levels in order to cope with the ***stress*** . Common features of the drought ***stress*** response in ***plants*** are the increase in abscisic acid (ABA) synthesis and accumulation in particular tissues and the synthesis of general and specific ***stress*** proteins. The understanding of the physiol. basis of drought ***stress*** response in cereals could benefit from the identification of ***gene*** functions involved in it. The strategies followed for the isolation of ***stress*** induced ***genes*** were both conventional and innovative. The conventional method was based on the prodn. and screening of a cDNA library, starting from coleoptiles of ABA-treated barley seedlings. Through a differential screening of these cDNAs it has been possible to isolate several ***genes*** encoding proteins with a protective role such as dehydrins, enzymes involved in the catabolism of drought ***stressed*** ***plants*** , such as aldose reductase and new functions specifically activated by the ***stress*** . Innovative methods, such as the RNA-differential display technique that allows the ***selection*** for and the display of a specific population of RNA mols. with a low level of abundance, were applied to obtain new and more specific cDNA clones. Several cDNA fragments were isolated from RNA populations obtained from ***plants*** subjected to different ***stress*** conditions. In many cases these cDNA fragments were revealed to be specific for some types of ***stress*** . These new clones are now being utilized for the isolation of complete cDNA and genomic clones possibly contg. ***genes*** characterized by a low level of expression and which may be good candidates for a ***regulative*** role in drought ***stress*** response.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 23 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:87563 CAPLUS
DN 128:201653
TI Molecular markers as aids to breeding more drought resistant crops
AU Quarrie, S. A.; Lazic-Jancic, Vesna; Ivanovic, M.; Pekic, Sofija; Lebreton, C.; Heyl, A.; Steed, A.; Calestani, C.
CS John Innes Centre, Norwich, UK
SO Drought and Plant Production, Proceedings [International Symposium], Lepenski Vir, Yugoslavia, Sept. 1996 (1997), Meeting Date 1996, Volume 2, 43-53. Editor(s): Jevtic, Stojan; Pekic, Sofija. Publisher: Agricultural Research Institute "Serbia", Belgrade, Yugoslavia. CODEN: 65OHAW
DT Conference
LA English
AB The development of mol. markers has made it much easier for physiologists to identify traits of importance for drought resistance and for breeders to identify the ***genes*** that ***regulate*** those responses to drought ***stress*** and help improve the drought resistance of new varieties. We have used mol. markers in rice and maize to identify quant. trait loci (QTL) for responses to drought ***stress*** . In one set of expts., we made a mol. map of the rice genome and used it to study the assocn. between the ability to produce the drought ***stress*** hormone abscisic acid (ABA) and leaf size in an F2 population. A mol. map of the maize genome was also made using an F2 population from a cross between two lines differing markedly in drought resistance (Polj17, resistant and F-2, susceptible). These ***plants*** and their F3 progenies were scored for a wide range of traits assocd. with drought resistance, such as phenol., root development, and ABA prodn., and QTLs for these traits compared with QTLs for yield. The comparison showed that flowering characteristics and nodal root no. were both likely to be important in detg. drought resistance. In a comparison of a CIMMYT maize population (Tuxpeno Sequia) before and after ***selection*** for high yield under drought, we used bulk segregant anal. to identify variation in allele frequencies between the two populations in several genomic regions, indicating the location of ***genes*** important for drought resistance. The application of this information to improving drought resistance in maize and other cereals is described.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 24 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:43552 CAPLUS
DN 128:125862
TI Ozone induction of ethylene emission in tomato ***plants*** : ***regulation*** by differential accumulation of transcripts for the biosynthetic enzymes
AU Tuomainen, Jaana; Betz, Christian; Kangasjarvi, Jaakko; Ernst, Dieter; Yin, Zu-Hua; Langebartels, Christian; Sandermann, Heinrich, Jr.
CS Dep. of Ecol. and Environ. Sci., Univ. of Kuopio, Kuopio, 70211, Finland
SO Plant Journal (1997), 12(5), 1151-1162 CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Science Ltd.
DT Journal
LA English
AB ***Stress*** ethylene emission is pos. correlated with ozone sensitivity in various ***plant*** species, indicating that ethylene may be involved in the control of ozone damage. Ozone exposure of tomato ***plants*** for 5 h at .gtoreq.85 nL L-1 leads to leaf injury within 24 h. 1-Aminocyclopropane-1-carboxylic acid (ACC) content and ACC synthase activity were accordingly elevated within 1-2 h. Pre-treatment of leaves with inhibitors of ACC synthase and ACC oxidase significantly inhibited the evolution of ethylene and reduced ozone-induced visible damage. Transcript levels for only one out of three S-adenosyl-L-methionine (SAM) synthetase ***genes*** (SAM3), and one out of four ACC synthase ***genes*** (LE-ACS2) were induced by ozone (max. at 2 h). Treatment with protein kinase (K-252a) and phosphatase inhibitors (calyculin A) revealed that ACC synthase activity was addnl. ***regulated*** by protein phosphorylation/dephosphorylation. Transcripts of ACC oxidase (pTOM13 cDNA probe) displayed the fastest response of the parameters tested (max. at 30 min), suggesting a ***regulatory*** role for ACC oxidase in ethylene formation of ozone-exposed ***plants*** . The results demonstrate a highly ***selective*** ozone response by ethylene biosynthetic ***genes*** which resembles that of ***plant*** -pathogen interactions.
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 25 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:26958 CAPLUS
DN 128:125896
TI An Arabidopsis mutant that requires increased calcium for potassium nutrition and salt tolerance
AU Liu, Jiping; Zhu, Jian-Kang

CS Dep. Plant Scis., Univ. Arizona, Tucson, AZ, 85721, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1997), 94(26), 14960-14964
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Potassium (K+) nutrition and salt tolerance are key factors controlling ***plant*** productivity. However, the mechanisms by which ***plants*** ***regulate*** K+ nutrition and salt tolerance are poorly understood. An Arabidopsis thaliana mutant, sos3 (salt-overly-sensitive 3), was identified which is hypersensitive to Na+ and Li+ ***stresses*** . The mutation is recessive and is in a nuclear ***gene*** that maps to chromosome V. The sos3 mutation also renders the ***plant*** unable to grow on low K+. Surprisingly, increased extracellular Ca2+ suppresses the growth defect of sos3 ***plants*** on low K+ or 50 mM NaCl. In contrast, high concns. of external Ca2+ do not rescue the growth of the salt-hypersensitive sos1 mutant on low K+ or 50 mM NaCl. Under NaCl ***stress*** , sos3 seedlings accumulated more Na+ and less K+/Na+ ***selectivity*** of both sos3 and wild-type ***plants*** . However, this Ca2+ effect in sos3 is more than twice as much as that in the wild type. In addn. to defining the first ***plant*** mutant with an altered calcium response, these results demonstrate that the SOS3 locus is essential for K+ nutrition, K+/Na+ ***selectivity*** , and salt tolerance in higher ***plants*** .
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 26 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:805840 CAPLUS
DN 128:71654
TI Tomato TWI1 glucosyltransferase and its ***plant*** homologs involved in ***plant*** defense and resistance
IN Bowles, Dianna Joy; O'Donnell, Philip James; Roberts, Michael Richard; Calvert, Caroline Mary
PA University of York, UK; Bowles, Dianna Joy; O'Donnell, Philip James; Roberts, Michael Richard; Calvert, Caroline Mary
SO PCT Int. Appl., 52 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 9745546 A1 19971204 WO 1997-GB1473 19970530 W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG AU 9729706 A1 19980105 AU 1997-29706 19970530 EP 914449 A1 19990512 EP 1997-924139 19970530 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
PRAI GB 1996-11420 19960531 WO 1997-GB1473 19970530
AB This invention relates to methods for inducing ***plant*** defense and resistance responses as well as ***regulating*** ***plant*** developmental events in monocots and dicots by modifying a ***gene*** encoding for a glucosyltransferase (TWI1) isolated from wounded tomatoes. Thus, the TWI1 glucosyltransferase ***gene*** was cloned and characterized from tomato, and used to identify sequences having substantial sequence homol. from tobacco and rice. Using the TWI1 cDNA sequence as a probe to analyze expression of the enzyme during a pathogen response in tomato, the ***gene*** was obsd. to be induced during ***gene*** -for- ***gene*** mediated resistance response involving the Cf9 R ***gene*** to Cladosporium fulvum. Similarly, using a homologous glucosyltransferase ***gene*** from tobacco as a probe, induction during ***gene*** -for- ***gene*** mediated R response involving the N ***gene*** to tobacco mosaic virus was obsd. Antisense technol. demonstrated that down- ***regulation*** of glucosyltransferase leads to prolonged levels of ***stress*** ethylene, and Northern anal. showed that a high expression of glucosyltransferase exists in senescence and in ripened fruits. The TWI1 promoter was activated following mech. wounding or pathogen attack. The glucosyltransferase can be used to (1) alter the signaling pathways of a ***plant*** involving salicylic acid, ethylene, and jasmonic acid, (2) inducing ***plant*** defense proteins, (3) ***regulating*** ***plant*** developmental events, and (4) stimulating or improving ***plant*** responses to pathogens.

L7 ANSWER 27 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:764657 CAPLUS
DN 128:32333
TI Improving salt tolerance of crop ***plants*** through tissue culture and molecular biology: progress and prospects
AU Winicov, Ilga
CS Departments of Microbiology and Biochemistry, University of Nevada at Reno, Reno, NV, 89557, USA
SO Proceedings of the Latvian Academy of Sciences, Section B: Natural, Exact and Applied Sciences (1997), 51(1/2), 19-27
CODEN: PLABFE; ISSN: 1407-009X
PB Latvian Academy of Sciences
DT Journal; General Review
LA English
AB A review with 109 refs. summarizing current progress in the understanding of cellular mechanisms important for achieving improved salt tolerance in crop ***plants*** , such as rice and alfalfa. This information is put in the context of other approaches undertaken to improve salt tolerance of ***plants*** and to elucidate the biol. mechanisms important in salt tolerance. Specific areas considered are as follows: (1) recent successful ***selection*** for salt tolerance in crop ***plants*** , by cell culture followed by regeneration of salt-tolerant ***plants*** , (2) the adaptive metabolic and physiol. responses to salt ***stress*** and their potential role in long term tolerance, (3) specific ***gene*** activation by salt, in view of proposed avenues for improved salt tolerance, (4) the need to ascertain the addnl. influences of hormonal and developmental ***regulation*** of ***gene*** expression in salt tolerance.
RE.CNT 110 THERE ARE 110 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 28 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:669722 CAPLUS
DN 127:315422
TI Molecular marker methods to dissect drought resistance in maize
AU Quarrie, S. A.; Lazic-Jancic, V.; Ivanovic, M.; Pekic, S.; Heyl, A.; Landi, P.; Lebreton, C.; Steed, A.
CS JOHN INNES CENTRE, NORWICH RESEARCH PARK, NORWICH, NR4 7UH, UK
SO Special Publication - Royal Society of Chemistry (1997), 209(Genetics, Biotechnology and Breeding of Maize and Sorghum), 52-58 CODEN: SROCDO; ISSN: 0260-6291

PB Royal Society of Chemistry
DT Journal
LA English
AB Qual. trait loci (QTL) anal. and bulk segregant anal. (BSA) were used to test the effect of abscisic acid (ABA) accumulation on drought resistance and to identify regions of the genome important in ***regulating*** drought resistance in the crop and traits likely to be assocd. with drought resistance. Tests were run on 2 composite populations of corn, with one population ***selected*** for yield under drought ***stress*** . QTL anal. of leaf ABA content identified 2 major QTLs on chromosomes 2 and 3, but there was no evidence from coincidence of QTLs that leaf ABA content affected yield. The BSA employed 28 RFLP probes to uncover major changes in allele frequency on chromosomes 1, 2, 3, 5, 6, 7, and 8 in respect to yield under drought conditions.

L7 ANSWER 29 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:478272 CAPLUS
DN 127:231870
TI ***Gene*** expression during cold acclimation in strawberry
AU Ndong, Christian; Ouellet, Francois; Houde, Mario; Sarhan, Fathey
CS Department des Sciences biologiques, Succursale "Centre-Ville", Universite du Quebec a Montreal, C.P. 8888, Montreal, QC, H3C 3P8, Can.
SO Plant and Cell Physiology (1997), 38(7), 863-870 CODEN: PCPHA5; ISSN: 0032-0781
PB Japanese Society of Plant Physiologists
DT Journal
LA English
AB To elucidate the mol. basis of cold acclimation in strawberry (Fragaria .times. anannassa), we have begun studies to identify ***genes*** assocd. with low temp. (LT) acclimation. Differential screening of a cDNA library prepd. from cold-acclimated strawberry ***plants*** allowed us to isolate several cDNAs showing differential expression at LT. Northern anal. showed that the transcript level of Fcor1 (Fragaria cold- ***regulated***) peaked after 2 days of LT exposure while that of Fcor2 peaked after 2 wk. On the other hand, the level of Fcor3 transcript decreased within 24 h of LT exposure and remained low during the 8 wk acclimation period. Fcor1 and Fcor2 are expressed in all tissues while Fcor3 is specific to leaves. The Fcor1-encoded protein has a compositional bias for leucine, isoleucine, glycine, proline and serine. This protein shares homol. with the proteins encoded by blt101, a LT-responsive ***gene*** from barley, and ESI3, a ***gene*** induced by salt ***stress*** in Lophopyrum. The FCOR2 protein is rich in lysine, leucine, valine, alanine and arginine, and shows no homol. with any known ***gene*** products. The partial Fcor3 cDNA clone encodes a polypeptide that shows a very high identity with the spinach PSI subunit V and with the PSI PsaG polypeptide from barley. The level of Fcor1 transcript accumulation is correlated with the freezing tolerance of the strawberry cultivars used in our study. This suggests that Fcor1 may be useful as a mol. marker to ***select*** for this trait in related species of the Rosaceae family.

L7 ANSWER 30 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:431442 CAPLUS
DN 127:133274
TI Molecular aspects of osmotic ***stress*** in ***plants***
AU Zhu, Jian-Kang; Hasegawa, Paul M.; Bressan, Ray A.
CS Department of Plant Sciences, University of Arizona, Tucson, AZ, 85721, USA
SO Critical Reviews in Plant Sciences (1997), 16(3), 253-277 CODEN: CRPSD3; ISSN: 0735-2689
PB CRC
DT Journal; General Review
LA English
AB A review with >100 refs. ***Plant*** mol. responses to osmotic ***stress*** are complex as evidenced by the isolation of numerous OR (osmotic ***stress*** - ***regulated***) ***genes*** . Although functions including osmolyte biosynthesis, membrane transport, signal transduction, and cellular protection have been predicted for OR ***genes*** , few of them have been established. Current efforts toward isolating and analyzing the expression of individual OR ***genes*** should be replaced by systematic approaches to analyze all OR ***genes*** simultaneously in ***selected*** ***plant*** species. Both transcriptional and posttranscriptional ***regulation*** of OR ***genes*** have been described. Cis-elements that respond to osmotic ***stress*** through abscisic acid (ABA)-dependent as well as ABA-independent pathways have been identified. Functional genetic approaches using yeast and ***plant*** model systems are expected to complement current mol. anal. of overexpression of OR ***genes*** in transgenic ***plants*** . These systems will help to establish functions of OR ***genes*** , to dissect osmotic ***stress*** -signaling pathways, and to det. crit. and rate-limiting cellular processes for osmotic ***stress*** tolerance. In this regard, initial results obtained through mutational anal. in Arabidopsis thaliana are promising and have identified novel salt-tolerant as well as salt-hypersensitive mutants.

L7 ANSWER 31 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:364689 CAPLUS
DN 127:63227
TI Abscisic acid and jasmonic acid activate wound-inducible ***genes*** in potato through separate, organ-specific signal transduction pathways
AU Dammann, Christian; Rojo, Enrique; Sanchez-Serrano, Jose J.
CS Centro Nacional de Biotecnologia CSIC, Campus Cantoblanco UAM, Madrid, 28049, Spain
SO Plant Journal (1997), 11(4), 773-782 CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell
DT Journal
LA English
AB Mech. damage to leaf tissue causes an increase in abscisic acid (ABA) which in turn activates the biosynthesis of jasmonic acid (JA). The resulting higher endogenous JA levels subsequently activate the expression of wound-inducible ***genes*** . JA induced the expression of different sets of ***genes*** in roots and leaves of potato ***plants*** . When roots of intact ***plants*** were treated with JA, high levels of proteinase inhibitor II (pin2), cathepsin D inhibitor, leucine aminopeptidase and threonine deaminase mRNAs accumulated in the systemic leaves. However, in the treated roots, very low, if any, expression of these ***genes*** could be detected. In contrast, a novel, root-specific pin2 homolog accumulated in the JA-treated root tissue which could not be detected in leaves, either systemic or those directly treated with JA. Application of okadaic acid and staurosporine revealed that a protein phosphorylation step is involved in the ***regulation*** of this differential response. In leaves, a protein phosphatase is required for the JA-induced expression of pin2 and the other ***genes*** analyzed. This

phosphatase activity is not necessary for the JA-induced expression of a pin2 homolog in roots, suggesting the existence of different transduction pathways for the JA signal in these organs. The requirement of a protein phosphatase activity for JA-mediated ***gene*** induction has enabled identification of a JA-independent pathway for ABA induction of pin2 and the other wound-inducible ***genes*** . This alternative pathway involves a protein kinase, and appears to be ***selective*** for wound-inducible ***genes*** . Thus, a complex, organ-specific transduction network ***regulates*** the effects of the ***plant*** hormones ABA and JA on ***gene*** expression upon wounding. RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 32 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:362568 CAPLUS
DN 127:106578
TI Metabolic implications of ***stress*** -induced proline accumulation in ***plants***
AU Hare, P. D.; Cress, W. A.
CS Natal University Research Unit Plant Growth Development, Department Botany, University Natal, Scottsville, 3209, S. Afr.
SO Plant Growth Regulation (1997), 21(2), 79-102 CODEN: PGRED3; ISSN: 0167-6903
PB Kluwer
DT Journal; General Review
LA English
AB A review with 179 refs. In many ***plants*** , free proline accumulates in response to the imposition of a wide range of biotic and abiotic ***stresses*** . Controversy has surrounded the extent to which this shift in nitrogen metab. benefits ***plants*** under adverse environmental conditions. Most attempts to account for the phenomenon have focused on the ability of proline to mediate osmotic adjustment, stabilize subcellular structures and scavenge free radicals. However, often the cytoplasmic pool of free proline even after the imposition of ***stress*** is insufficient size to account for pronounced biophys. effects. Alternatively, ***selective*** preservation of this ***stress*** -induced response may relate to endpoints other than simply augmenting the cellular pool of free proline. Proline accumulation may reduce ***stress*** -induced cellular acidification or prime oxidative respiration to provide energy needed for recovery. High levels of proline synthesis during ***stress*** may maintain NAD(P)+/NAD(P)H ratios at values compatible with metab. under normal conditions. Consideration of the cofactor preference of ***plant*** .DELTA.1-pyrroline-5-carboxylate (P5C) reductase as well as the in vivo concns. of the two pyridine nucleotide cofactors and their resp. redox ratios suggests that even a small increase in proline biosynthesis might have a large impact on the level of redn. of the cellular NADP pool. The increased NADP+/NADPH ratio mediated by proline biosynthesis is likely to enhance activity of the oxidative pentose phosphate pathway. This would provide precursors to support the demand for increased secondary metabolite prodn. during ***stress*** as well as nucleotide synthesis accompanying the accelerated rate of cell division upon relief from ***stress*** , when oxidn. of proline is likely to provide an important energy source for ADP phosphorylation. Thus, the extreme sensitivity of the metabolic processes of proline synthesis and degrdn. themselves may be of benefit by ***regulating*** metabolic processes adversely affected by ***stress*** . This viewpoint is supported by consideration of other physiol. phenomena not directly related to ***stress*** responses, but in which proline metab. may also play a ***regulatory*** role. A mechanism is proposed whereby the interconversions of proline and P5C in different cell types and the assocd. transfer of redox potential between tissues may constitute a form of metabolic signalling within higher ***plants*** . ***Stress*** -related alterations in proline metab. may impinge on systems of redox control of ***plant*** ***gene*** expression.

L7 ANSWER 33 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:336773 CAPLUS
DN 127:1247
TI QTL analysis of ***stress*** responses as a method to study the importance of ***stress*** -induced ***genes***
AU Quarrie, Steve; Heyl, Alexander; Steed, Andrew; Lebreton, Claude; Lazic-Jancic, Vesna
CS John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, UK
SO Physical Stresses in Plants: Genes and Their Products for Tolerance, Proceedings of the Workshop on Genes and Their Products for Tolerance to Physical Stresses in Plants, Maratea, Italy, Sept. 24-27, 1995 (1996), Meeting Date 1995, 141-152. Editor(s): Grillo, Stefania; Leone, Antonella. Publisher: Springer, Berlin, Germany. CODEN: 64JRAU
DT Conference; General Review
LA English
AB A review with 30 refs. Many ***genes*** are known to be activated in response to abiotic ***stresses*** . However, it is still not clear whether ***stress*** -activated ***gene*** products have a significant effect on improving the adaptation of crop ***plants*** to abiotic ***stresses*** . While transformation studies with ***stress*** -induced ***genes*** have shown some significant effects on specific physiol. processes, there is no evidence yet that the agronomic performance of crop ***plants*** can be improved using this approach. Mol. marker technologies, using restriction fragment length polymorphisms (RFLPs) and markers derived with polymerase chain reactions (PCR) allow high d. genetic maps to be prepd. These can be used to identify loci ***regulating*** expression of quant. traits (QTL). The candidate ***gene*** approach was used to study the possible roles of several ***stress*** -induced ***gene*** products. Coincidence of a QTL for a trait and a locus for a ***stress*** -induced ***gene*** could indicate a functional relation between the two. We mapped cDNAs for the maize rab17 and rab28 and rice rab16 ***genes*** in an F2 maize population and identified QTL for a wide range of responses to drought ***stress*** . However, no coincidence was found between the ***stress*** -induced cDNAs and QTL for ***stress*** responses or yield under drought. Using the bulked segregants C0 and C8 from the Tuxpeno Sequia population which differ markedly in yield under severe drought, several RFLP markers revealed changes in allele frequencies as a result of recurrent ***selection*** for yield under drought. Some of the RFLP probes showing changes in allele frequencies had homologies with ***genes*** likely to be involved in ***plant*** ***stress*** responses.

L7 ANSWER 34 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:54638 CAPLUS
DN 126:141956
TI New molecular tools to improve the efficiency of breeding for increased drought resistance
AU Quarrie, Stephen A.
CS John Innes Cent., Norwich Res. Park, Norwich, NR4 7UH, UK

SO Plant Growth Regulation (1996), 20(2), 167-178 CODEN: PGRED3; ISSN: 0167-6903
PB Kluwer
DT Journal; General Review
LA English
AB A review with 97 refs. The advent of mol. markers (particularly RFLP- and PCR-derived) for use as probes for genomic DNA has revolutionized the genetic anal. of crop ***plants*** and provided not only geneticists, but also physiologists, agronomists and breeders, with valuable new tools to identify traits of importance in improving resistance to abiotic ***stresses*** . For the breeder, a genetic map satd. with mol. markers allows ***selection*** for certain characters to be carried out much more efficiently and effectively than was possible previously. Two areas of mol. marker technol. that are proving particularly useful in identifying traits of value for ***stress*** resistance and introducing them into improved varieties are in situ hybridization with fluorescent-labeled mol. probes and quant. trait locus (QTL) anal. with either radioactively- or cold-labeled probes. Fluorescence in situ hybridization takes out much of the cytol. tedium previously assocd. with monitoring the introgression of chromosomes and DNA fragments from one species to another. Labeled DNA can be prepd. that is specific to a particular species and used to visualize in chromosome prepns. the presence of chromosomes or chromosomal fragments from that species amongst the recipient's chromosomes. This is being used to help transfer ***genes*** for drought resistance and sat tolerance from alien species into Graminaceous crops. DNA probes showing polymorphism between the donor and recipient species can also be used to monitor the incorporation of alien ***genes*** from chromosome addn. lines into the recipient species. High d. mol. maps allow the location of all major ***genes*** ***regulating*** the expression of a particular trait to be detd. Statistical methods have been developed to allow QTL for the trait to be identified. Not only does this allow the complexity of genetic control of any trait to be detd., but by comparing the extent to which confidence intervals of QTL for different traits overlap it is possible to exam. the likelihood that traits are pleiotropically linked. Thus, the traits most likely to be important in detg. yield under droughted conditions can be identified. Examples are given of traits that could be incorporated into breeding programs to improve drought resistance using techniques of marker-assisted ***selection*** .
RE.CNT 97 THERE ARE 97 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 35 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:25866 CAPLUS
DN 126:196083
TI Transcriptional and post-transcriptional activation of ***genes*** in salt-tolerant alfalfa cells
AU Winicov, Ilga; Krishnan, Muthu
CS Dep. Microbiology, Univ. Nevada, Reno, NV, 89557, USA
SO Planta (1996), 200(4), 397-404 CODEN: PLANAB; ISSN: 0032-0935
PB Springer
DT Journal
LA English
AB Salt-tolerant cell lines of alfalfa (Medicago sativa) ***selected*** in this lab. showed increased mRNA accumulation for both nuclear- and chloroplast-encoded ***genes*** involved in photosynthesis as well as in several non-photosynthetic related functions. The basis for this constitutive and salt-dependent ***gene*** activation was investigated by measuring both nuclear and plastid run-on transcription from the salt-sensitive parent line and from ***selected*** salt-tolerant lines. Plastids from tolerant cells showed a 2.5-fold increase in transcription rate over those from sensitive cells and a 4.5-fold increase if isolated from tolerant cells grown in salt. Nuclei isolated from salt-tolerant cells grown on normal medium showed higher transcription of the photosynthesis-related ***genes*** rbcS, cab1 and cab4 than those from salt-sensitive cells, confirming that the salt-tolerant cells had acquired altered transcriptional ***regulation*** of these ***genes*** . However, the major salt-induced increase in steady-state mRNA accumulation, from photosynthesis-related and other ***genes*** (alfin1, pA18 and histone H3cI and H3cII ***genes***), was not reflected in run-on assays from these same cells. These results indicated that salt-dependent post-transcriptional mRNA stabilization led to the steady-state mRNA accumulation. The mRNA stabilization appears to be transcript specific, since transcripts of a constitutively-expressed ***gene*** (Msc27) remained unaffected by growth of the tolerant cells in 171 mM NaCl.

L7 ANSWER 36 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:5250 CAPLUS
DN 126:85396
TI Identification of a light- ***regulated*** MYB ***gene*** from an Arabidopsis transcription factor ***gene*** collection
AU Quaedvlieg, Nicolette; Dockx, Jan; Keultjes, Gerbienne; Kock, Patriia; Wilmering, Jose; Weisbeek, Peter; Smeekens, Sjef
CS Dep. Mol. Cell Biol., Univ. Utrecht, Utrecht, 3584 CH, Neth.
SO Plant Molecular Biology (1996), 32(5), 987-993 CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer
DT Journal
LA English
AB Seven different MYB-related ***genes*** have been isolated from a genomic Arabidopsis library with probes based on MYB DNA-binding motifs. The predicted amino acid sequence of these ***genes*** showed high similarity in the MYB domain but outside this region virtually no similarities were found. The set of MYB-related ***genes*** was used to identify differentially expressed ***genes*** following the transfer of etiolated seedlings to light. This differential screen resulted in the ***selection*** of the ATM4 ***gene*** which is induced by light within one hour of exposure of etiolated or dark-adapted seedlings.

L7 ANSWER 37 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:716485 CAPLUS
DN 126:71846
TI Xanthophyll biosynthesis. Cloning, expression, functional reconstitution, and ***regulation*** of .beta.-cyclohexenyl carotenoid epoxidase from pepper (Capsicum annuum)
AU Bouvier, Florence; d'Harlingue, Alain; Hugueney, Philippe; Marin, Elena; Marion-Poll, Annie; Camara, Bilal
CS Inst. Biol. Mol., Univ. Louis Pasteur, Strasbourg, 67084, Fr.
SO Journal of Biological Chemistry (1996), 271(46), 28861-28867 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Pepper (Capsicum annuum) .beta.-cyclohexenyl xanthophyll epoxidase cDNA was cloned and the corresponding enzyme overexpressed and purified from Escherichia coli, for investigation of its catalytic activity. The

recombinant protein did not directly accept NADPH for epoxidn. of cyclohexenyl carotenoids, nor did it operate according to a peroxygenase-based mechanism. Instead, the reducing power of NADPH was transferred to the epoxidase via reduced ferredoxin as shown by reconstitution of epoxidase activity in the presence of NADPH, ferredoxin oxidoreductase, and ferredoxin. Bacterial rubredoxin could be substituted for ferredoxin. The pepper epoxidase acted specifically on the .beta.-ring of xanthophylls such as .beta.-cryptoxanthin, zeaxanthin, and antheraxanthin. The proposed reaction mechanism for epoxidn. involves the formation of a transient carbocation. This characteristic allows ***selective*** inhibition of the epoxidase activity by different nucleophilic diethylamine derivs., p-dimethylaminobenzenediazonium fluoroborate and N,N-dimethyl-2-phenylaziridinium. It was also shown that the epoxidase ***gene*** was up- ***regulated*** during oxidative ***stress*** and when chloroplasts undergo differentiation into chromoplasts in pepper fruit.

L7 ANSWER 38 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:607994 CAPLUS
DN 125:297294
TI Annexin-like protein from Arabidopsis thaliana rescues .DELTA.oxyR mutant of Escherichia coli from H2O2 ***stress***
AU Gidrol, Xavier; Sabelli, Paolo A.; Fern, Yip Soo; Kush, Anil K.
CS Inst. Mol. Cell Biol., Natl. Univ. Singapore, Singapore, 0511, Singapore
SO Proceedings of the National Academy of Sciences of the United States of America (1996), 93(20), 11268-11273 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Reactive oxygen species are common causes of cellular damages in all aerobic organisms. In Escherichia coli, the oxyR ***gene*** product is a pos. ***regulator*** of the oxyR regulon that is induced in response to H2O2 ***stress*** . To identify ***genes*** involved in counteracting oxidative ***stress*** in ***plants*** , we transformed a .DELTA.oxyR mutant of E. coli with an Arabidopsis thaliana cDNA library and ***selected*** for clones that restored the ability of the .DELTA.oxyR mutant to grow in the presence of H2O2. Using this approach, we isolated a cDNA that has strong homol. with the annexin super- ***gene*** family. The complemented mutant showed higher catalase activity. MRNA expression of the annexin ***gene*** in A. thaliana was higher in roots as compared with other organs and was also increased when the ***plants*** were exposed to H2O2 ***stress*** or salicylic acid. Based on the results presented in this study, we propose a novel physiol. role for annexin in counteracting H2O2 ***stress*** .

L7 ANSWER 39 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:574774 CAPLUS
DN 125:243179
TI Identification and expression of water ***stress*** - and abscisic acid- ***regulated*** ***genes*** in a drought-tolerant sunflower genotype
AU Ouvrard, Olivier; Cellier, Francoise; Ferrare, Karine; Tousch, Didier; Lamaze, Thierry; Dupuis, Jean-Marc; Casse-Delbart, Francine
CS Biochim. Physiol. Veg., CNRS, Montpellier, 34060, Fr.
SO Plant Molecular Biology (1996), 31(4), 819-829 CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer
DT Journal
LA English
AB We have studied two lines of sunflower (Helianthus annuus L.) ***selected*** in the field as drought-tolerant (R1 genotype) or drought-sensitive (S1 genotype). When subjected to drought conditions, the R1 line was able to maintain high leaf water potential longer and wilted later than the S1 line. Therefore, this indicates that R1 tolerance includes a leaf-adaptive response. By subtractive hybridization, we have isolated six different cDNAs (designated sdi for sunflower drought-induced) corresponding to transcripts accumulated in R1 and S1 leaves during adaptive response. Anal. of transcript accumulation in response to drought in both genotypes suggests a preferential expression of three sdi ***genes*** in the tolerant line. Abscisic acid-mediated induction, analyzed in R1 leaves, was obsd. for only four sdi ***genes*** . Sequence anal. of six sdi clones revealed that five clones were related to known proteins including non specific lipid transfer proteins (nsLTP), early light-induced proteins (ELIP), 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) or dehydrins, predicted to be involved in a wide range of physiol. processes.

L7 ANSWER 40 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:536054 CAPLUS
DN 125:190679
TI Salt ***stress*** -induced proline transporters and salt ***stress*** -repressed broad specificity amino acid permeases identified by suppression of a yeast amino acid permease-targeting mutant
AU Rentsch, Doris; Hirner, Brigitte; Schmelzer, Elmon; Frommer, Wolf B.
CS Institut Genbiologische Forschung, Berlin, D-14195, Germany
SO Plant Cell (1996), 8(8), 1437-1446 CODEN: PLCEEW; ISSN: 1040-4651
PB American Society of Plant Physiologists
DT Journal
LA English
AB A yeast mutant lacking SHR3, a protein specifically required for correct targeting of plasma membrane amino acid permeases, was used to study the targeting of ***plant*** transporters and as a tool to isolate new SHR3-independent amino acid transporters. For this purpose, an shr3 mutant was transformed with an Arabidopsis cDNA library. Thirty-four clones were capable of growth under ***selective*** conditions, but none showed homol. with SHR3. However, ***genes*** encoding eight different amino acid transporters belonging to three different transporter families were isolated. Five of these are members of the general amino acid permease (AAP) ***gene*** family, one is a member of the NTR family, encoding an oligopeptide transporter, and two beling to a new class of transporter ***genes*** . A functional anal. of the latter two ***genes*** revealed that they encode specific proline transporters (ProT) that are distantly related to the AAP ***gene*** family. ProT1 was found to be expressed in all organs, but highest levels were found in roots, stems, and flowers. Expression in flowers was highest in the floral stalk phloem that enters the carpels and was down- ***regulated*** after fertilization, indicating a specific role in supplying the ovules with proline. ProT2 transcripts were found ubiquitously throughout the ***plant*** , but expression was strongly induced under water or salt ***stress*** , implying that ProT2 plays an important role in nitrogen distribution during water ***stress*** , unlike members of the AAP ***gene*** family

whose expression was repressed under the same conditions. These results corroborate the general finding that under water ***stress*** , amino acid export is impaired whereas proline export is increased.

L7 ANSWER 41 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:365202 CAPLUS
DN 125:30118
TI Developmental and ***stress*** ***regulation*** of ***gene*** expression for plastid and cytosolic isoprenoid pathways in pepper fruits
AU Hugueney, Philippe; Bouvier, Florence; Badillo, Alfredo; Quennemet, Joelle; d'Harlingue, Alain; Camara, Bilal
CS Inst. Biol. Mol. Plantes Cent. Natl. Recherche Sci., Univ. Louis Pasteur, Strasbourg, 67084, Fr.
SO Plant Physiology (1996), 111(2), 619-626 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
AB ***Plant*** cells synthesize a myriad of isoprenoid compds. in different subcellular compartments, which include the plastid, the mitochondria, and the endoplasmic reticulum cytosol. To start the study of the ***regulation*** of these parallel pathways, pepper (Capsicum annuum) fruit was used as a model. Using different isoprenoid biosynthetic ***gene*** probes from cloned cDNAs, it was shown that only ***genes*** encoding the plastid enzymes (geranylgeranyl pyrophosphate synthase, phytoene synthase, phytoene desaturase, and capasanthin-capsorubin synthase) are specifically triggered during the normal period of development, at the ripening stage. This pattern of expression can be mimicked and precociously induced by a simple wounding ***stress*** . Concerning the cytosol-located enzymes, it was obsd. that the expression of the ***gene*** encoding farnesyl pyrophosphate synthase is constitutive, whereas that of farnesyl pyrophosphate cyclase (5-epi-aristolochene synthase) is undetectable during the normal development of the fruit. The expression of these later ***genes*** are, however, only ***selectively*** triggered after elicitor treatment. The results provide evidence for developmental control of isoprenoid biosynthesis occurring in plastids and that cytoplasmic isoprenoid biosynthesis is ***regulated*** , in part, by environmental signals.

L7 ANSWER 42 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:308890 CAPLUS
DN 124:338148
TI Application of quantitative trait locus mapping to the development of winter-habit malting barley
AU Oziel, A.; Hayes, P. M.; Chen, F. Q.; Jones, B.
CS Bean International Research and Development, Choisy-le-Roi, F-64600, Fr.
SO Plant Breeding (1996), 115(1), 43-51 CODEN: PLABED; ISSN: 0179-9541
PB Blackwell
DT Journal
LA English
AB Malting quality and winter-hardiness in barley are ultimate phenotypes composed of constituent quant. inherited traits. A synthesis of mol.-marker linkage data and field phenotyping to reveal the location of quant. trait loci (QTL) may assist in the development of winter-habit malting barley varieties. One-hundred doubled haploid progeny from a winter .times. spring cross were evaluated under fall and spring- ***planted*** conditions. Malting quality phenotypes and a 76-point map were used to identify QTL and to assess the effect of spring- and autumn-sowing on QTL expression. Many QTL effects were common to both environments and corresponded to QTL detected in other barley germplasm. While there were significant differences in the magnitude of effects across environments, there were no changes in the favorable allele phase. QTL effects for grain protein and diastatic power level coincided with the locations of known function ***genes*** . Coincident QTL for a no. of malting-quality traits on chromosome 7 suggests either the presence of a multi-locus cluster of ***genes*** controlling components of malting quality or a ***regulatory*** ***gene*** or ***genes*** controlling the cascade of enzymic processes that function during the malting process. Based on these results, simultaneous ***selection*** for malting quality and cold tolerance should be possible in this genetic background.

L7 ANSWER 43 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:290645 CAPLUS
DN 124:309565
TI Regeneration of genetically modified whole ***plant*** from ***plant*** cell transfected with DNA sequence comprising ***regulatory*** regions and ***genes*** for phenotype- ***regulating*** protein, recombinase, and genetic repressor
IN Oliver, Melvin John; Quisenberry, Jerry Edwin; Trolinder, Norma Lee Glover; Keim, Don Lee
PA Delta and Pine Land Company, USA; United States Dept. of Agriculture
SO PCT Int. Appl., 70 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 9604393 A2 19960215 WO 1995-US9595 19950731
WO 9604393 A3 19960307 W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TT, UA RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG US 5723765 A 19980303 US 1995-477559 19950607 AU 9532050 A1 19960304 AU 1995-32050 19950731 AU 696668 B2 19980917 EP 775212 A2 19970528 EP 1995-928199 19950731 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE BR 9508471 A 19971028 BR 1995-8471 19950731 JP 10503377 T2 19980331 JP 1995-506650 19950731
PRAI US 1994-283604 A 19940801 US 1995-477559 A 19950607 WO 1995-US9595 W 19950731
AB A method for making a genetically modified ***plant*** comprising regenerating a whole ***plant*** from a ***plant*** cell that has been transfected with DNA sequences comprising a first ***gene*** whose expression results in an altered ***plant*** phenotype linked to a transiently active promoter,the ***gene*** and promoter being sepd. by a blocking sequence flanked by specific excision sequences, a second ***gene*** that encodes a recombinase specific for the specific excision sequences linked to a repressible promoter, and a third ***gene*** that encodes the repressor specific for the repressible promoter. Also a method for making a genetically modified hybrid ***plant*** by hybridizing a first ***plant*** regenerated from a ***plant*** cell that has been transfected with DNA sequences comprising a first ***gene*** whose expression results in an altered ***plant*** phenotype linked to a transiently active promoter, the ***gene*** and promoter being sepd. by a blocking sequence flanked by specific

excision sequences to a second ***plant*** regenerated from a second ***plant*** cell that has been transfected with DNA sequences comprising a second ***gene*** that encodes a recombinase specific for the specific excision sequences linked to a promoter that is active during seed germination, and growing a hybrid ***plant*** from the hybrid seed. ***Plant*** cells, ***plant*** tissues, ***plant*** seed and whole ***plants*** contg. the above DNA sequences are also claimed.

L7 ANSWER 44 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:206574 CAPLUS
DN 124:255834
TI The SAL1 ***gene*** of Arabidopsis, encoding an enzyme with 3'(2'),5'-bisphosphate nucleotidase and inositol polyphosphate 1-phosphatase activities, increases salt tolerance in yeast
AU Quintero, Francisco J.; Garciadeblas, Blanca; Rodriguez-Navarro, Alonso
CS Dep. Biotecnologia, Univ. Politecnica de Madrid, Madrid, 28040, Spain
SO Plant Cell (1996), 8(3), 529-37 CODEN: PLCEEW; ISSN: 1040-4651
PB American Society of Plant Physiologists
DT Journal
LA English
AB A cDNA library in a yeast expression vector was prepd. from roots of Arabidopsis exposed to salt and was used to ***select*** Li+-tolerant yeast transformants. The cDNA SAL1 isolated from one of these transformants encodes a polypeptide of 353 amino acid residues. This protein is homologous to the HAL2 and CysQ phosphatases of yeast and Escherichia coli, resp. Partial cDNA sequences in the data bases indicate that rice produces a phosphatase highly homologous to SAL1 and that a second ***gene*** homologous to SAL1 exists in Arabidopsis. The SAl1 protein expressed in e. coli showed 3'(2'),5'-bisphosphate nucleotidase and inositol polyphosphate 1-phosphatase activities. In yeast, SAL1 restored the ability of a hal2/met22 mutant to grow on sulfate as a sole sulfur source, increased the intracellular LI+ tolerance, and modified Na+ and Li+ effluxes. We propose that the product of Sl1 participates in the sulfur assimilation pathway as well as in the phosphoinositide signaling pathway and that changes in the latter may affect Na+ and Li+ fluxes.

L7 ANSWER 45 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:77859 CAPLUS
DN 124:198205
TI A maize ***gene*** encoding an NADPH binding enzyme highly homologous to isoflavone reductases is activated in response to sulfur starvation
AU Petrucco, Stefania; Bolchi, Angelo; Foroni, Chiara; Percudani, Riccardo; Rossi, Gian Luigi; Ottonello, Simone
CS Institute Biochemical Sciences, University Parma, Parma, I-43100, Italy
SO Plant Cell (1996), 8(1), 69-80 CODEN: PLCEEW; ISSN: 1040-4651
PB American Society of Plant Physiologists
DT Journal
LA English
AB Sulfur nutrition plays an important role in the growth and development of higher ***plants*** , and glutathione, the main storage form of reduced sulfur, is involved in the response to a variety of ***stress*** conditions. The identification of ***genes*** activated on sulfur starvation may thus provide insights not only into the mechanisms of adaptation to nutrient limitation but also into the response(s) to ***stress*** resulting from glutathione depletion. By applying mRNA differential display anal. to a model system of maize seedlings grown hydroponically under either sulfate-sufficient or sulfate-deprived conditions, we isolated a novel ***gene*** that is ***selectively*** induced both in roots and shoots in response to sulfur starvation. This ***gene*** encodes a cytosolic, monomeric protein of 33 kDa that ***selectively*** binds NADPH. The predicted polypeptide is highly homologous (>70%) to leguminous isoflavone reductases (IFRs), but the maize protein (IRL for isoflavone reductase-like) belongs to a novel family of proteins present in a variety of ***plants*** . Anti-IRL antibodies specifically recognize IFR polypeptides, yet the maize protein is unable to use various isoflavonoids as substrates. IRL expression is correlated closely to glutathione availability: it is persistently induced in seedlings whose glutathione content is about fourfold lower than controls, and it is down- ***regulated*** rapidly when control levels of glutathione are restored. This glutathione-dependent ***regulation*** indicates that maize IRL may play a crucial role in the establishment of a thiol-independent response to oxidative ***stress*** under glutathione shortage conditions.

L7 ANSWER 46 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:42934 CAPLUS
DN 124:78720
TI ***Gene*** wilt ***regulating*** the response of Zea mays to water deficit
IN Chomet, Paul; Dellaporta, Stephen L.; Orr, Peter; Krueger, Roger W.; Lowe, Brenda A.
PA Dekalb Genetics Corp., USA; Yale University
SO PCT Int. Appl., 77 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 9530005 A1 19951109 WO 1995-US5366 19950428 W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TT, UA RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG CA 2190597 AA 19951109 CA 1995-2190597 19950428 AU 9523714 A1 19951129 AU 1995-23714 19950428 AU 697810 B2 19981015 ZA 9503474 A 19960410 ZA 1995-3474 19950428 EP 759076 A1 19970226 EP 1995-917777 19950428 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE
PRAI US 1994-235060 A 19940429 WO 1995-US5366 W 19950428
AB The present invention involves the identification and characterization of ***genes*** involved in the response of maize ***plants*** to water ***stress*** . A mutant allele of the wilt ***gene*** was identified by transposon tagging and demonstrated to correlate with a mutants phenotype of wilting under normal water conditions.

L7 ANSWER 47 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:41589 CAPLUS
DN 124:137229
TI Novel ***plant*** Ca2+-binding protein expressed in response to abscisic acid and osmotic ***stress***
AU Frandsen, Gitte; Mueller-Uri, Frieder; Nielsen, Michael; Mundy, John; Skriver, Karen
CS Institute of Molecular BIology, Copenhagen Univ., Copenhagen K, Den.

SO Journal of Biological Chemistry (1996), 271(1), 343-48 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB A cDNA corresponding to an mRNA which accumulates in germinating rice seeds in response to the phytohormone abscisic acid was isolated by differential hybridization. Northern blotting indicated that the mRNA also accumulates in vegetative tissues in response to treatment with abscisic acid and to osmotic ***stress*** . Sequencing identified a major open reading frame encoding a novel protein of 27.4 kDa. The identity of the open reading frame was confirmed by comparing the translation products of cellular, hybrid-***selected*** , and in vitro transcribed RNAs and by immunopptn. Western blotting of cellular exts. indicated that the protein is assocd. with microsomal or membrane fractions. Data base searches indicated that it contains a conserved Ca2+-binding, EF-hand motif and that related proteins are similarly expressed in Arabidopsis thaliana. A fusion protein purified from Escherichia coli contg. the putative EF-hand region was shown to bind Ca2+ in blot binding assays. These data identify a novel ***gene*** family encoding proteins involved in the response of ***plants*** to abscisic acid and osmotic ***stress*** .

L7 ANSWER 48 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:892722 CAPLUS
DN 123:310286
TI Molecular aspects of heterosis in ***plants***
AU Tsaftaris, S. Athanasios
CS Dep. Genet. Plant Breeding, Aristotelian Univ. Thessaloniki, Thessaloniki, G-54 006, Greece
SO Physiologia Plantarum (1995), 94(2), 362-70 CODEN: PHPLAI; ISSN: 0031-9317
PB Munksgaard
DT Journal; General Review
LA English
AB A review with 60 refs. Since Shull's original description of heterosis, breeders have made wide use of this phenomenon. However, while agronomists have been utilizing heterosis as a means of improving crop productivity, the biol. basis of heterosis remains unknown. It is generally believed that the understanding of heterosis will enhance the ability to form new genotypes which may be used directly as F1 hybrids or form the basis for future ***selection*** programs. While the original concept of heterosis resulted from studies at the phenotypic morphol. level, they were soon followed by biochem. data with the advent of electrophoresis and the consequent ease of accumulation of data related to isoenzyme variability. However, the large no. of restriction fragment length polymorphisms from more recent studies has allowed the development of linkage maps with a high degree of resoln. useful in locating and manipulating quant. trait loci (QTL). When substantial nos. of such neutral markers were used to measure genetic distance in large nos. of maize inbreds, very significant correlations were recorded between parental genetic distance and hybrid performance. Through the same approach, a relatively small no. of QTLs dispersed through the maize genome were identified which show clear overdominance expression controlling heterosis. The hypothesis was made that some QTLs could code for ***regulatory*** proteins since these proteins are able to control a vast array of other structural ***genes*** , the products of which are necessary for the expression of complicated characters such as yield and heterosis for yield. The few such proteins identified thus far are all multimeric proteins with the heteropolymers exhibiting significantly different activities in comparison with the homopolymers, that is in compliance with the clear overdominance manifestation of the few QTLs analyzed so far. In addn., parameters derived from the variability of genome expression assessed through studies of polymorphisms in the amts. of individual proteins or mRNAs show numerous significant correlations between these indexes and hybrid vigor. These correlations supported the conclusion that QTLs could be loci controlling the amt. of mRNAs or proteins synthesized from a no. of structural ***genes*** , and ***stress*** the significance of both the ***regulatory*** proteins (and their encoding ***genes***) and the structural ***genes*** , being ***regulated*** , in manifestation of complicated characters, such as heterosis.

L7 ANSWER 49 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:301837 CAPLUS
DN 122:153266
TI The ocs element in the soybean GH2/4 promoter is activated by both active and inactive auxin and salicylic acid analogs
AU Ulmasov, Tim; Hagen, Gretchen; Guilfoyle, Tom
CS Department of Biochemistry, Univ. of Missouri, Columbia, MO, 65211, USA
SO Plant Molecular Biology (1994), 26(4), 1055-64 CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer
DT Journal
LA English
AB The octopine synthase (ocs or ocs-like) element has been previously reported to be responsive to the ***plant*** hormones, auxin, salicylic acid, and Me jasmonate. Transient assays with carrot protoplasts were used to demonstrate that an ocs element from the soybean auxin-inducible GH2/4 promoter is not only activated by strong auxins (i.e., 2,4-dichlorophenoxyacetic acid, 2,4,5-trichlorophenoxyacetic acid, .alpha.-naphthaleneacetic acid) and salicylic acid, but also by weak auxin analogs (.beta.-naphthaleneacetic acid), inactive auxin analogs (i.e., 2,3-dichlorophenoxyacetic acid, 2,4,6-trichlorophenoxyacetic acid), and inactive salicylic acid analogs (3-hydroxybenzoic acid and 4-hydroxybenzoic acid). The results indicate that the ocs element in the GH2/4 promoter is not ***selectively*** induced by ***plant*** hormones and might function similarly to tandem AP-1 sites in some animal glutathione S-transferase (GST) ***genes*** . The ocs element, like the AP-1 sites in animal GST promoters, may be induced not only by certain hormones but also by some non-hormonal ***stress*** -inducing or electrophilic agents.

L7 ANSWER 50 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:44701 CAPLUS
DN 122:2346
TI Expressed sequence tags from cultured cells of rice (Oryza sativa L.) under ***stressed*** conditions: analysis of transcripts of ***genes*** engaged in ATP-generating pathways
AU Umeda, Masaaki; Hara, Chikage; Matsubayashi, Yuko; Li, Hai-Hang; Liu, Qiang; Tadokoro, Fumihiko; Aotsuka, Satoshi; Uchimiya, Hirofumi
CS Inst. Mol. Cellular Biosci., Univ. Tokyo, Tokyo, 113, Japan
SO Plant Molecular Biology (1994), 25(3), 469-78 CODEN: PMBIDB; ISSN: 0167-4412
DT Journal
LA English
AB Large-scale sequencing of randomly ***selected*** cDNA clones was used to isolate numerous ***genes*** in rice (Oryza sativa L.). Total RNA used for cDNA synthesis was

prepd. from suspension-cultured cells of rice grown under ***stressed*** conditions, such as in saline or nitrogen-starvation conditions. A total of 780 cDNA clones were partially sequenced and about 15% could be identified as putative ***genes*** . In the library constructed under saline conditions, the authors identified several ***genes*** assocd. with signal transduction, such as protein kinase and small GTP-binding protein ***genes*** . Many ***stress*** -related ***genes*** were isolated from both the saline and nitrogen-starvation libraries. These results indicate that ***stress*** treatment of suspension-cultured cells makes it possible to efficiently isolate various types of ***plant*** ***genes*** . To examine the usefulness of such tagged cDNAs for the study of ***gene*** expression in a specific metabolic pathway, the authors analyzed mRNA levels of ***genes*** engaged in the ATP-generating pathways in cultured cells of rice under different ***stresses*** , such as 20% sucrose, salt ***stress*** , cold ***stress*** and nitrogen-starvation ***stress*** . The results suggest that the coordinated induction of several ***genes*** in key steps under ***stressed*** conditions may be essential for activation of the entire energy-producing pathway to maintain homeostasis in rice cells. Expressed sequence tags identified by random cDNA sequencing provide the opportunity to generate a transcript map of rice ***genes*** .

L7 ANSWER 51 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:24573 CAPLUS
DN 122:152756
TI Cloning of cDNAs for ***genes*** that are specifically or preferentially expressed during the development of tobacco genetic tumors
AU Fujita, Tomomichi; Kouchi, Hiroshi; Ichikawa, Takanari; Syono, Kunihiko
CS Department Pure and Applied Sciences, University Tokyo, Meguro, 153, Japan
SO Plant Journal (1994), 5(5), 645-54 CODEN: PLJUED; ISSN: 0960-7412
DT Journal
LA English
AB To identify ***genes*** involved in the formation of genetic tumors in interspecific hybrids (F1) between Nicotiana glauca and N. langsdorffii, genetic tumor-related cDNA probes were obtained by a subtractive hybridization procedure and used to screen libraries of genetic tumor cDNAs. As a result, 17 distinct cDNA clones were isolated for ***genes*** that are specifically or preferentially expressed in genetic tumor tissues but are not expressed at all or are barely expressed in normal F1 ***plants*** . Among the isolated clones were ***genes*** that encoded so-called ***stress*** proteins, such as glucan endo-1,3-.beta.-glucosidase, osmotin, pathogenesis-related proteins and proteinase inhibitor I. Transcripts corresponding to two of the isolated cDNA clones accumulated to a significant extent only in genetic tumor tissues and were not present in callus tissues from parental ***plants*** or in the stems and leaves from normal F1 ***plants*** . Anal. of genomic DNA revealed that four of these clones hybridized only to genomic sequences from N. langsdorffii and one hybridized only to a genomic sequence from N. glauca. Eight apparently novel clones were further analyzed to det. the kinetics of accumulation of the corresponding mRNAs during development of genetic tumors. The patterns of accumulation of the mRNAs after induction of tumors by cutting of F1 stems could be divided into three groups, an indication that at least three distinct ***regulatory*** mechanisms are operative at the transcriptional level to control the expression of these tumor-related ***genes*** during the formation of genetic tumors.

L7 ANSWER 52 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:17933 CAPLUS
DN 122:73425
TI Hsr203J, a tobacco ***gene*** whose activation is rapid, highly localized and specific for incompatible ***plant*** /pathogen interactions
AU Pontier, Dominique; Godiard, Laurence; Marco, Yves; Roby, Dominique
CS Lab. Biol. Mol. Relations Plantes/Microorg., CNRS, Castanet-Tolosan, 31326, Fr.
SO Plant Journal (1994), 5(4), 507-21 CODEN: PLJUED; ISSN: 0960-7412
DT Journal
LA English
AB A novel ***plant*** defense ***gene*** , hsr 203J, whose corresponding mRNA accumulates preferentially during the incompatible interaction of tobacco (Nicotiana tabacum L.) with a pathogenic bacterium, Pseudomonas solanacearum, has been isolated and sequenced. No sequence homol. of the putative product of this ***gene*** has been found in data bases. Evidence is presented here that the hsr 203J ***gene*** promoter, when fused to the GUS reporter ***gene*** , is ***selectively*** expressed in response to the hypersensitive response (HR)-inducing bacteria in tobacco protoplasts and that the sequences responsible for this response are contained within 1.4 kb of the 5' noncoding region. The temporal and spatial patterns of hsr 203J activation in leaves and roots inoculated with P. solanacearum indicate that the hsr 203J promoter exhibits a rapid (3-6 h post-inoculation) and high level of induction only in ***plant*** cells inoculated with the HR-inducing bacterial isolate. In addn., this ***gene*** promoter which does not respond to various ***stress*** conditions and is only very weakly induced during compatible interactions, is strongly dependent on hrp (hypersensitive response and pathogenicity) ***genes*** of P. solanacearum. These data indicate that the hsr 203J ***gene*** promoter exhibits new and original characteristics of activation with regard to the ***plant*** defense ***genes*** studied so far; its spatial and temporal program of activation together with its specific induction during the HR underline the importance of this ***gene*** as a mol. tool for studying the establishment and ***regulation*** of the HR.

L7 ANSWER 53 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1994:647715 CAPLUS
DN 121:247715
TI A deoxygenase ***gene*** (Ids2) expressed under iron deficiency conditions in the roots of Hordeum vulgare
AU Okumura, Nami; Nishizawa, Naoko-Kishi; Umehara, Yosuke; Ohata, Tomoko; Nakanishi, Hiromi; Yamaguchi, Takahiro; Chino, Mitsuo; Mori, Satoshi
CS Lab. Plant Nutr. Fertilizer, Univ. Tokyo, Bunkyo-ku, Tokyo, 113, Japan
SO Plant Molecular Biology (1994), 25(4), 705-19 CODEN: PMBIDB; ISSN: 0167-4412
DT Journal
LA English
AB A .lambda.zapII cDNA library was constructed from mRNA isolated from Fe-deficient barley roots and screened with cDNA probes made from mRNA of Fe-deficient and Fe-sufficient (control) barley roots. Seven clones were ***selected*** . Among them a clone having the putative full-length mRNA of dioxygenase as judged by northern

hybridization was ***selected*** and named Ids2 (iron deficiency-specific clone 2). Using a cDNA fragment as probe, two clones from the genomic library (.lambda.EMBL-III) were isolated and one was sequenced. The predicted amino acid sequence of Ids2 resembled that of 2-oxoglutarate-dependent dioxygenase. Ids2 is expressed in the Fe-deficient barley roots but is not in the leaves. The expression is repressed by the availability of Fe. Ids2 was also strongly expressed under Mn deficiency and weakly under Zn deficiency or excess NaCl(0.5%). The upstream 5'-flanking region of Ids2 has a root-specific cis element of the CaMV 35S promoter and a nodule-specific element of legHb, a metal ***regulatory*** element (MRE) and several Cu ***regulatory*** elements (UAS) of yeast metallothionein (CUP1).

L7 ANSWER 54 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1994:504924 CAPLUS
DN 121:104924
TI Mammalian mitogen-activated protein kinase kinase kinase (MEKK) can function in a yeast mitogen-activated protein kinase pathway downstream of protein kinase C
AU Blumer, Kendall J.; Johnson, Gary L.; Lange-Carter, Carol A.
CS Sch. Med., Washington Univ., St. Louis, MO, 63110, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1994), 91(11), 4925-9 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB Mitogen-activated protein kinase cascades are conserved in fungal, ***plant*** , and metazoan species. The authors expressed murine MAP kinase kinase kinase (MEKK) in the yeast Saccharomyces cerevisiae to det. whether this kinase functions as a general or specific activator of genetically and physiol. distinct MAP-kinase-dependent signaling pathways and to investigate how MEKK is ***regulated*** . Expression of MEKK failed to correct the mating deficiency of a ste11.DELTA. mutant that lacks an MEKK homolog required for mating. MEKK expression also failed to induce expression of a reporter ***gene*** controlled by the HOG1 ***gene*** product (Hog1p), a yeast MAP kinase homolog involved in response to osmotic ***stress*** . Expression of MEKK did correct the cell lysis defect of a bck1.DELTA. mutant that lacks an MEKK homolog required for cell-wall assembly. MEKK required the downstream MAP kinase homolog in the BCK1-dependent pathway, demonstrating that it functionally replaces the BCK1 ***gene*** product (Bck1p) rather than bypassing the pathway. MEKK therefore ***selectively*** activates one of three distinct MAP-kinase-dependent pathways. Possible explanations for this ***selectivity*** are discussed. Expression of the MEKK catalytic domain, but not the full-length mol., cor. the cell-lysis defect of a pkc1.DELTA. mutant that lacks a protein kinase C homolog that functions upstream of Bck1p. MEKK therefore functions downstream of the PKC1 ***gene*** product (Pkc1p). The N-terminal noncatalytic domain of MEKK, which contains several consensus protein kinase C phosphorylation sites, may, therefore, function as a neg. ***regulatory*** domain. Protein kinase C phosphorylation may provide one mechanism for activating MEKK.

L7 ANSWER 55 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1994:184499 CAPLUS
DN 120:184499
TI Analysis of a desiccation and ABA-responsive promoter isolated from the resurrection ***plant*** Craterostigma ***plantagineum***
AU Michel, Detlef; Salamini, Francesco; Bartels, Dorothea; Dale, Phyllis; Baga, Monica; Szalay, Aladar
CS Max Planck Inst. Zuechtungsforsch., Cologne, D-5000, Germany
SO Plant Journal (1993), 4(1), 29-40 CODEN: PLJUED; ISSN: 0960-7412
DT Journal
LA English
AB The resurrection ***plant*** Craterostigma ***plantagineum*** can recover from severe desiccation within 24 h of contact with water, and it is used as a model system to analyze desiccation tolerance in higher ***plants*** . During drying or ABA treatment a specific set of transcripts accumulates rapidly in leaves and other tissues. In order to study transcriptional mechanisms of ***stress*** -induced ***gene*** expression one ***gene*** (CDeT27-45) was ***selected*** for promoter anal. Chimeric ***gene*** fusions were constructed of the CDeT27-45 promoter and .beta.-glucuronidase or luciferase. These constructs were tested in a homologous transient expression system which allowed the identification of promoter elements conferring ABA inducibility. By introducing the chimeric ***gene*** fusions into tobacco via Agrobacterium-mediated transformation the authors found that the promoter activity is under strict tissue-specific and developmental control. In tobacco the promoter was only active in developing embryos and in mature pollen grains -- two tissues which are naturally desiccation tolerant in tobacco. The specific temporal expression pattern was attributed to particular 5' upstream sequences. The promoter anal. presented here should allow the sepn. of important ***regulatory*** components as a first step in dissecting events in the signal transduction chain.

L7 ANSWER 56 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1994:70583 CAPLUS
DN 120:70583
TI Molecular cloning and sequence analysis of cDNAs encoding cytoplasmic low molecular weight heat shock proteins in hexaploid wheat
AU Weng, Jian; Wang, Zi Fen; Nguyen, Henry T.
CS Plant Mol. Genet. Lab., Texas Tech Univ., Lubbock, TX, 79409, USA
SO Plant Science (Shannon, Ireland) (1993), 92(1), 35-46 CODEN: PLSCE4; ISSN: 0168-9452
DT Journal
LA English
AB Heat shock proteins (HSPs) are known to accumulate in ***plants*** under high temps. ***stress*** conditions. In an effort to study the function of low-mol.-wt. (LMW) HSPs in cultivated wheat, the authors have cloned and characterized 3 cDNAs from Triticum aestivum, Tahsp16.9A, Tahsp16.9B, and Tahsp17.4, resp., that encoded peptides having homol. to the cytoplasmic LMW HSP family. Nucleotide sequence comparison indicate that: Tahsp16.9A and Tahsp16.9B belong to the LMW HSP class I; there is 82% identity of whole cDNA sequence between them, but only 58% identity at the 3' non-conding region. Tahsp17.4 belongs to LMW HSP class II. Amino acid sequence comparisons indicate that there is a 97% similarity between Tahsp16.9 and Tashp16.9B and 57% between class I and class II (Tahsp17.4) members in wheat. There is a 93% similarity between Tashp17.4 and Zmhsp17.9 from maize which belong to class II of LMW HSPs. Northern blot hybridization anal. was performed using poly(A)+ RNA from green leaf tissues treated at different temps. (25.degree., 28.degree., 31.degree., 34.degree., 37.degree. and 40.degree.) for 60 min or at 37.degree. for different time periods (0, 7.5, 15, 30, 60, 120, and 240 min). These expts.

revealed that the expression of Tahsp16.9B and Tahsp17.4 was induced beginning at 31.degree. and reached max. levels at 37.degree.. The onset of mRNA induction occurred within about 7 min, reached a peak at 60 min and declined after 240 min when treated under the optimal heat ***stress*** condition (37.degree.). In vitro hybrid ***selection*** and Southern blot anal. data indicate that Tahsp16.9A and Tahsp16.9B belong to a 12-member class I multigene family. Tahsp 17.4 on the other hand belongs to a 14-member class II multigene family. These cDNAs, which encode cytoplasmic LMW HSPs in hexaploid wheat, will provide the authors with tools to investigate the roles of HSPs in an agriculturally important cereal crop species.

L7 ANSWER 57 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1994:27629 CAPLUS
DN 120:27629
TI Diverse genetic responses to environmental ***stress*** in a salt-tolerant ***plant*** : Classes of transcripts
AU Cushman, John C.; Derocher, E. Jay; Vernon, Daniel M.; Thomas, John C.; Michalowski, Christine B.; Bohnert, Hans J.
CS Dep. Biochem., Univ. Arizona, Tucson, AZ, 85721, USA
SO Res. Photosynth., Proc. Int. Congr. Photosynth., 9th (1992), Volume 4, 195-202. Editor(s): Murata, Norio. Publisher: Kluwer, Dordrecht, Neth. CODEN: 59IZA5
DT Conference
LA English
AB The authors present a few ***selected*** topics illustrating different types of ***stress*** -adaptive responses that act synergistically to form the basis of the ice ***plant*** 's (Mesembryanthemum crystallinum) tolerance to environmental ***stresses*** . The sections indicate that (1) the photosynthetic app. is largely protected against the effects of ***stress*** as judged by the expression of ***genes*** for photosynthetic-related functions, (2) CAM induction gives rise to long-term protection by providing a highly water use efficient mode of nocturnal and carbon uptake and fixation, (3) polyol prodn. is the major protection mechanism against osmotic ***stress*** both long and short term, and (4) root-specific changes in ***gene*** expression in response to salinity ***stress*** may make a major contribution towards the ability of this facultative halophyte to withstand osmotic ***stress*** . Various environmental ***stresses*** , depending on the agent producing the osmotic ***stress*** and other environmental conditions (such as light intensity and quality) affect a very large no. of ***genes*** , whose expression is up- ***regulated*** , maintained, or down- ***regulated*** . It is proposed that many of these changes in ***gene*** expression, including down- ***regulation*** , have adaptive significance. By using a direct screening approach, the authors est. the magnitude of changes in ***gene*** expression to be on the order of 100-200 ***genes*** up- ***regulated*** and about 3 times this no. down- ***regulated*** in response to salt ***stress*** . Part of the ***gene*** expression changes that are shown here exemplify the flexibility of the ice ***plant*** in coping with different ***stresses*** in different ways. Some responses are dependent on the tissue type, the cell type, and/or the developmental status of the ***plant*** . It will be important in the future to focus on cell specificity of ***stress*** responses, how specific responses are integrated in tissues, and how communication is achieved between organs (for example, the root and leaf systems).

L7 ANSWER 58 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:622041 CAPLUS
DN 119:222041
TI ***Regulatable*** induction of male sterility in ***plants*** .
IN Fabijanski, Steven F.; Albani, Diego; Robert, Laurian S.; Arnison, Paul G.
PA Paladin Hybrids Inc., Can.
SO Can. Pat. Appl., 240 pp. CODEN: CPXXEB
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI CA 2021643 AA 19920121 CA 1990-2021643 19900720
PRAI CA 1990-2021643 19900720
AB Male sterility is induced by preventing expression of a ***gene*** involved in pollen development. An antisense transcript of the ***gene*** is used to prevent translation. Pollen-specific expression of an heterologous ***gene*** for an enzyme that will convert a nontoxic precursor to a toxic product are also used. The antisense transcript need not be controlled by a pollen-specific promoter if the sense transcript is pollen-specific. Methods for restoration of the activity inhibited by the antisense transcript are described. Tobacco carrying the .beta.-glucuronidase (GUS) ***gene*** under control of the cauliflower mosaic virus 35S promoter were transformed with the vector PAL 1302 carrying an antisense transcription unit for the GUS ***gene*** . Transformants showed a lower GUS activity, that was correlated with a lowering of the concn. of material cross-reacting with antibody to GUS.

L7 ANSWER 59 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:599543 CAPLUS
DN 119:199543
TI Characterization of two maize HSP90 heat shock protein ***genes*** : expression during heat shock, embryogenesis, and pollen development
AU Marrs, Kathleen A.; Casey, Elena Silva; Capitant, Sherry A.; Bouchard, Robert A.; Dietrich, Paul S.; Mettler, Irvin J.; Sinibaldi, Ralph M.
CS Plant Biotechnol. Dep., Sandoz Agro, Inc., Palo Alto, CA, 94304, USA
SO Developmental Genetics (New York, NY, United States) (1993), 14(1), 27-41 CODEN: DGNTDW; ISSN: 0192-253X
DT Journal
LA English
AB The authors isolated two ***genes*** from Zea mays encoding proteins of 82 and 81 kD that are highly homologous to the Drosophila 83-kD heat shock protein ***gene*** and have analyzed the structure and pattern of expression of these two ***genes*** during heat shock and development. Southern blot anal. and hybrid ***select*** translations indicate that the highly homologous hsp82 and hsp81 ***genes*** are members of a small multigene family composed of at least two and perhaps three or more ***gene*** family members. The deduced amino acid sequence of these proteins based on the nucleotide sequence of the coding regions shows 64-88% amino acid homol. to other hsp90 family ***genes*** from human, yeast, Drosophila, and Arabidopsis. The promoter regions of both the hsp82 and hsp81 ***genes*** contain several heat shock elements (HSEs), which are putative binding sites for heat shock transcription factor (HSF) commonly found in the promoters of other heat shock ***genes*** . ***Gene*** -specific oligonucleotide probes were synthesized and used to examine the mRNA expression patterns of the hsp81 and hsp82 ***genes*** during heat shock, embryogenesis, and pollen development. The hsp81 ***gene*** is only mildly heat inducible in leaf tissue, but is strongly expressed in the

absence of heat shock during the pre-meiotic and meiotic prophase stages of pollen development and in embryos, as well as in heat-shocked embryos and tassels. The hsp82 ***gene*** shows strong heat inducibility at heat-shock temps. (37-42.degree.) and in heat shocked embryos and tassels but is only weakly expressed in the absence of heat shock. Promoter-GUS reporter ***gene*** fusions made and analyzed by transient expression assays in Black Mexican Sweet (BMS) Maize protoplasts also indicate that the hsp82 and hsp81 are ***regulated*** differentially. The hsp82 promoter confers strong heat-inducible expression of the GUS reporter ***gene*** in heat-treated cells (60- to 80-fold over control levels), whereas the hsp81 promoter is only weakly heat inducible (5- to 10-fold over control levels).

L7 ANSWER 60 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:403568 CAPLUS
DN 119:3568
TI Stilbene synthase from Scots pine (Pinus sylvestris)
AU Schanz, Sigrid; Schroeder, Gudrun; Schroeder, Joachim
CS Inst. Biol. II, Univ. Freiburg, Freiburg, D-7800, Germany
SO FEBS Letters (1992), 313(1), 71-4 CODEN: FEBLAL; ISSN: 0014-5793
DT Journal
LA English
AB Stilbene synthases are named according to their substrate preferences. By this definition, enzymes preferring cinnamoyl-CoA are pinosylvin synthases, and proteins with a preference for phenylpropionyl-CoA are dihydropinosylvin synthases. The assignment of a stilbene synthase cloned from Scots pine (P. sylvestris) as dihydropinsoylvin synthase and the proposal of an addnl. pinosylvin synthase were investigated. The results show that the previous interpretation was complicated by several unexpected factors. First, the substrate preference and the activity of the ***plant*** -specific protein expressed in Escherichia coli were influenced by bacterial factors. This was reduced by improvement of the expression system, and the subsequent kinetic anal. revealed that cinnamoyl-CoA rather than phenylpropionyl-CoA is the preferred substrate of the cloned stilbene synthase. Second, mixing expts. showed that exts. from P. sylvestris contain factor(s) which ***selectively*** influenced the substrate preference, i.e. the activity was reduced with phenylpropionyl-CoA, but not with cinnamoyl-CoA. This explained the apparent differences between ***plant*** exts. and the cloned enzyme expressed in E. coli. Taken together, the results indicate that the cloned enzyme is a pinosylvin synthase, and there is no evidence for a second stilbene synthase. This study cautions that factors in the natural and in new hosts may complicate the functional identification of cloned sequences.

L7 ANSWER 61 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:248693 CAPLUS
DN 118:248693
TI High frequency, heat treatment-induced inactivation of the phosphinothricin resistance ***gene*** in transgenic single cell suspension cultures of Medicago sativa
AU Walter, Christian; Broer, Inge; Hillemann, Doris; Puehler, Alfred
CS Fak. Biol., Univ. Bielefeld, Bielefeld, W-4800, Germany
SO Molecular and General Genetics (1992), 235(2-3), 189-96 CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB One descendant of the M. sativa Ra-3 transformant T304 was analyzed with respect to the somatic stability of the synthetic phosphinothricin-N- acetyltransferase (pat) ***gene*** which was used as a ***selective*** marker and was under the control of the 5'/3' expression signals of the cauliflower mosaic virus (CaMV) ***gene*** VI. In order to quantify ***gene*** instability, a system was developed for culturing and regenerating individual cells. Single cell suspension cultures derived from T304 and the ancestral non-transgenic M. sativa cultivar Ra-3, were established. The cells were regenerated into monoclonal calli. In transgenic calli, the phosphinothricin (Pt)-resistance phenotype was retained after more than 2 mo of non- ***selective*** growth. In contrast, up to 12% of the suspension culture cells grown under nonselective conditions and at const. temp. (25.degree.) lost the herbicide-resistance phenotype within 150 days. Surprisingly, a heat treatment (37.degree.), lasting for 10 days, during the culture period resulted in an almost complete (95%) loss of the Pt resistance of the suspension culture cells. However, the frequency of cell division was identical in cultures grown under normal and heat treatment conditions. A biochem. test revealed that no phosphinothricin-N-acetyltransferase activity was present in the heat treated, Pt-sensitive cells. The resistance level of the Pt-sensitive transgenic cells was equiv. to that of the wild-type cells. A PCR anal. confirmed the presence of the pat ***gene*** in heat treated, Pt-sensitive cells. From these results it is concluded that the Pt resistance ***gene*** was heat-inactivated at a high frequency in the M. sativa suspension cultures.

L7 ANSWER 62 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:143530 CAPLUS
DN 118:143530
TI ***Regulation*** of plastid ***gene*** expression during photooxidative ***stress***
AU Tonkyn, John C.; Deng, Xing Wang; Gruissem, Wilhelm
CS Dep. Plant Biol., Univ. California, Berkeley, CA, 94720, USA
SO Plant Physiology (1992), 99(4), 1406-15 CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
AB The carotenoid biosynthesis inhibitor norflurazon was used to study the relationship between chloroplast and nuclear ***gene*** expression and the mechanisms by which plastid mRNA accumulation is ***regulated*** in response to photooxidative ***stress*** . In 4-wk-old hydroponic spinach ***plants*** (Spinacea oleracea), differences were found between the norflurazon-treated young and mature leaves. Young leaves lost essentially all pigment content in the presence of norflurazon, whereas mature leaves retained >60% of their chlorophyll and carotenoids. The accumulation of plastid mRNA was detd. for several ***genes*** , and mRNA levels decreased for all ***genes*** except psbA in herbicide-treated young leaves. For ***genes*** such as atpB, psbB, and psaA, there was a corresponding change in the relative level of transcription, but for psbA and rbcL, transcription and mRNA accumulation were uncoupled. In norflurazon-treated mature leaves, all plastid mRNAs except psaA accumulated to normal levels, and transcription levels were either normal or higher than corresponding controls. Thus, plastid mRNA accumulation is ***regulated*** both transcriptionally and posttranscriptionally in response to photooxidative ***stress*** . Although direct photooxidative damage is confined to the plastid and peroxisome, there is a feedback of information controlling the transcription of nuclear-encoded plastid proteins. Considerable evidence has accumulated implicating a plastid factor in this control. Therefore, the expression of several nuclear-encoded plastid proteins and the corresponding mRNAs were detd. Although

the levels of both the small subunit of ribulose-1,5-bisphosphate carboxylase and the light harvesting chlorophyll a/b-binding protein and corresponding mRNAs were reduced, a 28-kilodalton chloroplast RNA-binding protein and corresponding mRNA were at normal levels in norfluorazon-treated ***plants*** . Changes in mRNA and protein levels were not the result of a general loss due to photooxidn. but rather the result of ***selective*** stabilization of certain components. The response of both genomes to photooxidative ***stress*** is discussed in terms of the postulated plastid factor.

L7 ANSWER 63 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:77007 CAPLUS
DN 118:77007
TI Emerging strategies for enhancing crop resistance to microbial pathogens
AU Lamb, Christopher J.; Ryals, John A.; Ward, Eric R.; Dixon, Richard A.
CS Plant Biol. Lab., Salk Inst. Biol. Stud., La Jolla, CA, 92037, USA
SO Bio/Technology (1992), 10(11), 1436-45 CODEN: BTCHDA; ISSN: 0733-222X
DT Journal; General Review
LA English
AB A review with 123 refs. There are marked differences in the pattern of host ***gene*** expression in incompatible ***plant*** : microbial pathogen interactions compared with compatible interactions, assocd. with the elaboration of inducible defenses. Constitutive expression of ***genes*** encoding a chitinase or a ribosome-inactivating protein in transgenic ***plants*** confers partial protection against fungal attack, and a large repertoire of such antimicrobial ***genes*** has been identified for further manipulation. In addn., strategies are emerging for the manipulation of multigenic defenses such as lignin deposition and synthesis of phytoalexin antibiotics by overexpression of ***genes*** encoding rate detg. steps, modification of transcription factors or other ***regulatory*** ***genes*** , and engineering prodn. of novel phytoalexins by interspecies transfer of biosynthetic ***genes*** . The imminent cloning of disease resistance ***genes*** , further mol. dissection of ***stress*** signal perception and transduction mechanisms, and identification of ***genes*** that affect symptom development will provide attractive new opportunities for enhancing crop protection. Combinatorial integration of these novel strategies into ongoing breeding programs should make an important contribution to effective, durable field resistance.

L7 ANSWER 64 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:1697 CAPLUS
DN 118:1697
TI The Arabidopsis HSP-18.2 promoter/GUS ***gene*** fusion in transgenic Arabidopsis ***plants*** : a powerful tool for the isolation of ***regulatory*** mutants of the heat-shock response
AU Takahashi, Taku; Naito, Satoshi; Komeda, Yoshibumi
CS Mol. Genet. Res. Lab., Univ. Tokyo, Tokyo, 113, Japan
SO Plant Journal (1992), 2(5), 751-61 CODEN: PLJUED; ISSN: 0960-7412
DT Journal
LA English
AB A detailed study of the expression of the promoter of the HSP18.2 ***gene*** from Arabidopsis fused to the bacterial ***gene*** for .beta.-glucoronidase (GUS) in transgenic Arabidopsis ***plants*** is described. High levels of GUS activity were induced in all organs of transformants except for seeds during heat shock. The optimum temp. for expression of GUS in Arabidopsis was 35.degree. regardless of the ***plant*** growth temp. Heat shock of 40.degree. did not induce any detectable levels of GUS activity. Pre-incubation at 35.degree. was found to have a protective effect on the induction of GUS activity at 40.degree.. GUS activity was also increased in response to a gradual increase in temp. Histochem. anal. revealed that basal levels of GUS activity were induced in the vascular tissue of leaves and sepals, as well as at the tips of carpels, at the normal growth temp. Heat treatment of a limited part of the ***plant*** tissue did not appear to cause systemic induction of GUS activity. To extend the anal. of the ***plant*** heat-shock response, the authors attempted to screen mutations in ***genes*** involved in the ***regulation*** of the induction of heat-shock protein (HSP) ***genes*** , using the GUS ***gene*** as a ***selection*** marker in transgenic Arabidopsis ***plants*** , and the results of this anal. are described.

L7 ANSWER 65 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1992:547343 CAPLUS
DN 117:147343
TI A molecular marker to ***select*** for freezing tolerance in Gramineae
AU Houde, Mario; Dhindsa, Rajinder S.; Sarhan, Fathey
CS Dep. Sci. Biol., Univ. Quebec, Montreal, QC, H3C 3P8, Can.
SO Molecular and General Genetics (1992), 234(1), 43-8 CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB The authors isolated, and expressed in Escherichia coli, a ***gene*** (Wcs120) that is strongly induced during cold acclimation of wheat. The ***gene*** product was purified and used to produce antibodies. Immunoblotting expts. with the anti-WCS120 antibody identified several cold-influenced proteins named FTMs for Freezing Tolerance Markers since they are assocd. with the development of freezing tolerance. This protein family was found to be coordinately ***regulated*** specifically by low temp., highly hydrophilic, stable to boiling, and to have a pI above 6.5. The accumulation kinetics during the acclimation period indicated a pos. correlation with the capacity of each genotype to develop freezing tolerance. Accumulation of the proteins was higher in the freezing-tolerance genotype than in the less tolerant one. In addn., their accumulation was more pronounced in the crown and leaf tissues compared with roots, confirming a relationship to the capacity of the different tissues to develop freezing tolerance. Anal. of different species (eight monocots and four dicots) indicated that this protein family is specific for freezing-tolerant cereals. The antibody did not cross-react with any of the non-cereal species examd. The anti-FTMs antibody represents a potential tool for breeders to ***select*** for freezing tolerance traits in the Gramineae.

L7 ANSWER 66 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1992:487057 CAPLUS
DN 117:87057
TI Agrobacterium-mediated transformation and regeneration of chrysanthemum ***plants***
IN Lemieux, Christine S.
PA Florigene, B. V., Neth.
SO PCT Int. Appl., 47 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 9203041 A1 19920305 WO 1991-US5805 19910815 W: AU, JP, US RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE AU 9184330 A1 19920317 AU 1991-84330 19910815 US 5567599 A 19961022 US 1994-251392 19940126
PRAI US 1990-570575 19900821 WO 1991-US5805 19910815
AB Methods for Agrobacterium-mediated transformation of chrysanthemum explants are demonstrated. Sterile explants are inoculated with a suspension of A. tumefaciens, carrying the transforming DNA, and after transformation, the explant is transferred to a regeneration medium. Explants may be first cultivated on a cytokinin-contg. medium and after transformation placed on a regeneration medium contg. an antibiotic active against Agrobacterium. Transformation of several cultivars of Dendranthema grandiflora with a neomycin phosphotransferase ***gene*** under control of the 35S promoter was demonstrated.

L7 ANSWER 67 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1992:466710 CAPLUS
DN 117:66710
TI Nitrogen-dependent ***regulation*** of the ***gene*** for alanine aminotransferase which is involved in the C4 pathway of Panicum miliaceum
AU Son, Daeyoung; Kobe, Atsuto; Sugiyama, Tatsuo
CS Sch. Agric., Nagoya Univ., Nagoya, 464-01, Japan
SO Plant and Cell Physiology (1992), 33(4), 507-9 CODEN: PCPHA5; ISSN: 0032-0781
DT Journal
LA English
AB Levels of protein and mRNA for alanine aminotransferase, which is involved in the C4 pathway of P. miliaceum, were measured during recovery from N deficiency ***stress*** . The enzyme accumulates ***selectively*** in response to N availability primarily as a consequence of changes in the level of its mRNA.

L7 ANSWER 68 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1992:252225 CAPLUS
DN 116:252225
TI Effects of nitrate and ammonium on ***gene*** expression of phosphoenolpyruvate carboxylase and nitrogen metabolism in maize leaf tissue during recovery from nitrogen ***stress***
AU Sugiharto, Bambang; Sugiyama, Tatsuo
CS Sch. Agric., Nagoya Univ., Nagoya, 464-01, Japan
SO Plant Physiology (1992), 98(4), 1403-8 CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
AB The ***selective*** accumulation of phosphoenolpyruvate carboxylase (PEPC) in photosynthetically maturing maize (Zea mays) leaf cells induced by nitrate supply to nitrogen-starved ***plants*** was primarily a consequence of the level of its mRNA (B. Sugiharto et al; 1990). To det. the specificity of inorg. nitrogen sources for the ***regulation*** of PEPC ***gene*** expression, nitrate (16 mM) or ammonium (6 mM) was supplied to ***plants*** grown previously in low nitrate (0.8 mM), and changes in the level of PEPC and its mRNA were measured in the basal region of the youngest, fully developed leaves of ***plants*** during recovery from nitrogen ***stress*** . The exogenous supply of nitrogen ***selectively*** increased the levels of protein and mRNA for PEPC. This increase was more pronounced in ***plants*** supplemented with ammonium than with nitrate. The accumulation of PEPC during nitrogen recovery increased in parallel with the increase in the activity of glutamine synthetase and/or ferredoxin-dependent glutamate synthase. Among the major amino acids, glutamine was the most influenced during recovery, and its level increased in parallel with the steady-state level of PEPC mRNA for 7 h after nitrogen supply. The administration of glutamine (12 mM) to nitrogen-starved ***plants*** increased the steady-state level of PEPC mRNA 7 h after administration, whereas 12 mM glutamate decreased the level of PEPC mRNA. The results indicate that glutamine and/or its metabolite(s) can be a pos. control on the nitrogen-dependent ***regulation*** of PEPC ***gene*** expression in maize leaf cells.

L7 ANSWER 69 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1991:676084 CAPLUS
DN 115:276084
TI Sodium chloride ***regulation*** of tonoplast ATPase 70-kilodalton subunit mRNA in tobacco cells
AU Narasimhan, Meena L.; Binzel, Marla L.; Perez-Prat, Eva; Chen, Zutang; Nelson, Donald E.; Singh, Narendra K.; Bressan, Ray A.; Hasegawa, Paul M.
CS Cent. Plant Environ. Stress Physiol., Purdue Univ., West Lafayette, IN, 47907, USA
SO Plant Physiology (1991), 97(2), 562-8 CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
AB A cDNA clone encoding the 70-kilodalton subunit of the tobacco (Nicotiana tabacum var Wisconsin 38) tonoplast ATPase has been isolated. The 1.656 kilobase insert contains only open reading frame that represents >80% of the carrot cDNA coding region. The deduced amino acid sequence has >95% sequence identity with the homologous carrot sequence. A transcript of approx. 2.7 kilobase was detected on Northern blots of tobacco poly(A)+ ***selected*** or total RNA using labeled probe produced from this clone. The ***gene*** was expressed throughout the growth cycle in unadapted and 428 mM NaCl adapted cells. Transcription of the 70-kilodalton subunit ***gene*** or mRNA stability was induced by short-term NaCl treatment in NaCl adapted cells or by abscisic acid treatment in both adapted and unadapted cells. Southern anal. indicated the presence of up to four ***genes*** encoding the 70-kilodalton subunit.

L7 ANSWER 70 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1991:137343 CAPLUS
DN 114:137343
TI Transformation of Japanese potato cultivars with the .beta.-glucuronidase ***gene*** fused with the promoter of the pathogenesis-related 1a protein ***gene*** of tobacco
AU Ishige, Teruo; Ohshima, Masahiro; Ohashi, Yuko
CS Natl. Inst. Agrobiol. Resourc., Tsukuba, 305, Japan
SO Plant Science (Shannon, Ireland) (1991), 73(2), 167-74 CODEN: PLSCE4; ISSN: 0168-9452
DT Journal
LA English
AB A fragment of the pathogenesis-related protein 1a (PR1a) ***gene*** of tobacco was introduced into Japanese potato cultivars by Agrobacterium-mediated ***gene*** transfer using the binary vector system. A PR1a promoter/.beta.-glucuronidase (GUS) fusion ***gene*** was used to study the expression of the ***gene*** after salicylic acid treatment. Transformed shoots were recovered from tuber disks using a kanamycin resistant ***gene*** as a ***selective*** marker. Transformants were obtained from 11 cultivars including leading Japanese varieties. Southern blot anal. of transformants revealed that a DNA probe for the GUS coding region hybridized with nuclear DNA of transformants and the copy no. of introduced ***gene*** was different

among transformants. The transformants having the GUS reporter ***gene*** fused with the PR1a promoter showed high GUS activity after salicylic acid treatment. The level of GUS ***gene*** expression was almost as high as in transformed potatoes having a GUS ***gene*** fused with the CaMV-35S promoter. Wide variation in the level of ***gene*** expression among regenerated transformants was obsd. The inducible expression of tobacco PR1a ***gene*** in transformed potato cultivars showed that the promoter of the PR1a ***gene*** is valuable for potato improvement and is capable of driving the expression of target ***genes*** under ***stress*** conditions.

L7 ANSWER 71 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1991:96107 CAPLUS
DN 114:96107
TI Direct screening of a small genome: estimation of the magnitude of ***plant*** ***gene*** expression changes during adaptation to high salt
AU Meyer, Gabriele; Schmitt, Juergen M.; Bohnert, Hans J.
CS Dep. Biochem., Univ. Arizona, Tucson, AZ, 85721, USA
SO Molecular and General Genetics (1990), 224(3), 347-56 CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB Mesembryanthemum crystallinum (common ice ***plant***), a facultative halophyte with a genome size of 393,000 kb, was used to est. the magnitude of changes in ***gene*** expression in response to environmental ***stress*** by excess salt. Such treatment induces a water-conserving pathway of carbon assimilation (CAM) which is, at least in part, transcriptionally controlled. From a genomic library, 200 phage contg. approx. 3200 kb (0.8% of the genome) were randomly ***selected*** . The inserts in these clones could be divided into 4 classes ranging from highly repetitive DNA (class I clones) to single-copy DNA (class IV clones). The inserts of the 166 clones of classes II to IV were digested with various restriction enzymes and the fragments were analyzed by hybridization with radioactively labeled mRNA isolated from ***stressed*** and unstressed leaves. A total of .apprx.140 DNA fragments hybridized with the RNA probe. Among those, several differentially ***regulated*** transcripts were obsd. ***Stress*** -dependent fluctuation of mRNA abundance was verified by Northern anal.: one mRNA, not detectable in unstressed leaves, appeared in ***stressed*** leaves, whereas steady-state levels of 3 transcripts decreased during ***stress*** . All ***regulated*** signals are derived from low abundance mRNAs, which may be missed during screening of cDNA libraries. It was concluded from these results that, for the entire genome, >100 ***genes*** are differentially ***regulated*** in response to salt ***stress*** .

L7 ANSWER 72 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1990:608548 CAPLUS
DN 113:208548
TI Characterization of three mRNAs that accumulate in wilted tomato leaves in response to elevated levels of endogenous abscisic acid
AU Cohen, Amybeth; Bray, Elizabeth A.
CS Dep. Bot. Plant Sci., Univ. California, Riverside, CA, 92521, USA
SO Planta (1990), 182(1), 27-33 CODEN: PLANAB; ISSN: 0032-0935
DT Journal
LA English
AB The accumulation of abscisic acid (ABA) has been shown to ***regulate*** some of the changes in ***gene*** expression which occur during water deficit. To characterize these ABA-induced changes, three copy DNAs (cDNAs) were identified and isolated. They represent ***genes*** which are expressed in response to ABA during drought ***stress*** . The ABA-deficient mutant of tomato, flacca, synthesizes low levels of ABA during water deficit compared to the wild type (WT) Lycopersicon esculentum. The mutant flacca was used to distinguish cDNAs corresponding to mRNAs which accumulate during water deficit in response to elevated levels of ABA from those mRNAs which are not ABA responsive. A cDNA library representing the mRNA population of wilted WT tomato leaves was constructed and a series of differential screens was used to ***select*** cDNAs that represent putative ABA- and drought-induced mRNAs. Three cDNAs were isolated from the screens and were identified as pLE4, pLE16, and pLE25. The corresponding mRNAs were preferentially expressed in wilted WT leaves and were not expressed in wilted ABA-deficient mutant leaves. The inability of the mutant to accumulate these drought-induced transcripts was reversed with exogenously applied ABA. A correlation was obsd. between the accumulation of the drought-induced mRNAs and the endogenous ABA levels measured in WT leaves throughout increasing periods of water deficit. These results indicate that endogenous ABA ***regulates*** the accumulation of pLE4, pLE16, and pLE25 mRNAs in tomato leaves during water deficit.

L7 ANSWER 73 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1990:546442 CAPLUS
DN 113:146442
TI Induced expression of a chimeric ***gene*** construct in transgenic lettuce ***plants*** using tobacco pathogenesis-related protein ***gene*** promoter region
AU Enomoto, Sueo; Itoh, Hirotaka; Ohshima, Masahiro; Ohashi, Yuko
CS Natl. Inst. Agrobiol. Resour., Tsukuba, 305, Japan
SO Plant Cell Reports (1990), 9(1), 6-9 CODEN: PCRPD8; ISSN: 0721-7714
DT Journal
LA English
AB The expression of a ***stress*** - and salicylic acid-inducible protein ***gene*** from tobacco, the PR1a protein ***gene*** , was detd. after its introduction into lettuce (Lactuca sativa L.) ***plants*** . The 5'-flanking 2.4-kb fragment from PR1a ***gene*** was joined to the bacterial .beta.-glucuronidase (GUS) ***gene*** (PR-GUS) and introduced into lettuce cotyledons by Agrobacterium-mediated ***gene*** transfer using a binary vector contg. a kanamycin-resistance ***gene*** as a ***selectable*** marker. As a control with constitutive expression, the chimeric ***gene*** consisting of cauliflower mosaic virus 35 S RNA promoter and GUS ***gene*** (35 S-GUS) was used. An improved method for shoot formation directly from lettuce cotyledons was used effectively for transformation, shortening the time for regeneration. In 70% or more of kanamycin-resistant regenerated lettuce ***plants*** , into which PR-GUS or 35 S-GUS was introduced, high GUS activity and integration of the chimeric ***gene*** into the lettuce genome were detected. By treatment with salicylic acid, GUS activity increased 3- to 50-fold in PR-GUS transformants, however, no increase was detected in 35 S-GUS ***plants*** . These results showed that the promoter of the ***stress*** -inducible tobacco PR1a protein ***gene*** was introduced into lettuce ***plants*** , and the introduced chimeric

gene was expressed normally under the ***regulated*** control of the PR1a promoter.

L7 ANSWER 74 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1990:403363 CAPLUS
DN 113:3363
TI ***Regulation*** of expression of carbon-assimilating enzymes by nitrogen in maize leaf
AU Sugiharto, Bambang; Miyata, Kazuya; Nakamoto, Hitoshi; Sasakawa, Hideo; Sugiyama, Tatsuo
CS Sch. Agric., Nagoya Univ., Nagoya, 464-01, Japan
SO Plant Physiology (1990), 92(4), 963-9 CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
AB The cellular differentiation gradient of the developed, youngest leaf was used to exam. the ***regulation*** by nitrogen of levels of phosphoenolpyruvate carboxylase (PEPCase), pyruvate orthophosphate dikinase (PPDK), and ribulose 1,5-diphosphate carboxylase in corn (Zea mays). The protein ***regulated*** most preferentially by N availability was PEPCase, followed by PPDK, and the changes in content occurred most conspicuously in the photosynthetically maturing cells. Pulse and pulse-chase expts. to analyze photosynthetic fixation of [14C]CO2 indicate that corn leaf primarily exploited a C4-mode of photosynthetic fixation of carbon dioxide even under a ***selective*** redn. in levels of these proteins. The effects of N on the synthesis of these proteins and the accumulation of corresponding mRNAs during recovery from a deficiency were examd. by pulse and pulse-chase labeling with [35S]methionine and by hybridization, resp. The rate of of turnover of PPDK was substantially higher than that of the other proteins. Results also showed that the reduced accumulation of PEPCase, as well as PPDK, under N deficiency could largely be accounted for a reduced level of synthesis of protein with a concomitant redn. in level of their mRNAs. This indicates that the N-dependent ***selective*** accumulation of these enzymes is primarily a consequence of level of its mRNAs.

L7 ANSWER 75 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:611864 CAPLUS
DN 111:211864
TI Genetic and molecular evidence of abiotic ***stress*** resistance in cereals
AU Marmiroli, N.; Perrotta, C.; Di Cola, G.; Terzi, V.; Stanca, A. M.
CS Biol. Dep., Univ. Lecce, Italy
SO Chimica Oggi (1989), 7(4), 51-4 CODEN: CHOGDS; ISSN: 0392-839X
DT Journal; General Review
LA English
AB A review with 54 refs. in which some important trends in the improvement of cereals with respect to their response to environmental ***stresses*** such as heat, cold, anaerobiosis, anoxia, and drought are discussed. Addnl. topics include: the impact of the genotype on the environment, ***regulation*** of ***gene*** expression during environmental ***stress*** , and ***selection*** procedures for ***stress*** tolerance.

L7 ANSWER 76 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:528152 CAPLUS
DN 111:128152
TI Differential ***regulation*** of phenylalanine ammonia-lyase ***genes*** during ***plant*** development and by environmental cues
AU Liang, Xiaowu; Dron, Michel; Cramer, Carole L.; Dixon, Richard A.; Lamb, Christopher J.
CS Salk Inst. Biol. Stud., Univ. California, San Diego, La Jolla, CA, 92037, USA
SO Journal of Biological Chemistry (1989), 264(24), 14486-92 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Phenylalanine ammonia-lyase (PAL) catalyzes the 1st reaction in the biosynthesis from phenylalanine of a wide variety of phenylpropanoid natural products including lignin, flavonoid pigments, and phytoalexins. In bean (Phaseolus vulgaris L.), PAL is encoded by a family of 3 ***genes*** . RNase protection with ***gene*** -specific probes showed that these ***genes*** are expressed differentially during development and in response to different environmental cues. Whereas all 3 ***genes*** are expressed at high levels in roots, only PAL1 and PAL2 are expressed in shoots and only PAL1 is expressed in leaves. Strikingly, PAL2 is expressed at very high levels in petals, whereas PAL1 is only very weakly expressed and PAL3 is not expressed. All 3 ***genes*** are induced by mech. wounding of hypocotyls, but fungal infection only activates PAL1 and PAL3. Illumination of etiolated hypocotyls activates PAL1 and PAL2 but not PAL3. Corresponding differential patterns of synthesis of specific PAL polypeptide isoforms were obsd. by 2-dimensional gel electrophoretic anal. of in vitro translation products encoded by RNA isolated from hypocotyls stimulated by light, wounding, or infection. The specific isoforms encoded by transcripts of the 3 PAL ***genes*** were identified by inhibition of synthesis in vitro with ***gene*** -specific anti-sense transcripts followed by comparative 2-dimensional gel electrophoretic anal. of the pattern of translation products. These data indicate that ***selective*** expression of PAL ***genes*** encoding functional variants is governed by a complex set of ***regulatory*** networks for developmental and environmental control of phenylpropanoid biosynthesis.

L7 ANSWER 77 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:510194 CAPLUS
DN 111:110194
TI Sequence analysis and transcriptional ***regulation*** by heat shock of polyubiquitin transcripts from maize
AU Christensen, Alan H.; Quail, Peter H.
CS Univ. California, Berkeley, CA, 94720, USA
SO Plant Molecular Biology (1989), 12(6), 619-32 CODEN: PMBIDB; ISSN: 0167-4412
DT Journal
LA English
AB A maize ubiquitin cDNA clone was isolated which encodes one partial and 3 full-length, identical 76 amino acid repeats in a polyprotein conformation. The deduced amino acid sequence of the mature monomeric polypeptide is identical to that detd. for 3 other ***plants*** , barley, oat, and Arabidopsis, and differs from yeast and animal ubiquitin by only 2 and 3 amino acids, resp. Hybridization of the cDNA clone to restriction endonuclease-digested genomic DNA revealed that ubiquitin is encoded by a small multigene family in maize. Northern blot anal. of poly(A)+ RNA indicated that multiple ubiquitin mRNAs of 2.1, 1.6, and 0.8 kb are produced in maize shoots and roots. The abundance of the largest (2.1 kb) of these transcripts increased transiently 3-4-fold over the first 1 to 3 h in seedlings that were subjected to heat shock, and then returned dramatically within 1 h almost to the preshocked level. In contrast, the 2 smaller transcripts showed little or no change following heat shock. Run-on transcription assays in isolated maize nuclei showed a heat shock-induced

increase in ubiquitin run-on transcripts that paralleled the increase in mature 2.1 kb mRNA levels over the first 3 h following the heat shock treatment. This result indicates that heat shock ***regulates*** ubiquitin ***gene*** expression at least in part at the transcriptional level. The subsequent rapid decline in steady-state mRNA levels, on the other hand, was not preceded by decreased ubiquitin ***gene*** transcription, raising the possibility of both transcriptional and posttranscriptional ***regulation*** . The run-on transcription assays also revealed a transient 5-fold redn. in rRNA ***gene*** transcription following heat shock, indicating that the transcriptional machinery for these ***genes*** is ***selectively*** sensitive to this ***stress*** .

L7 ANSWER 78 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:494012 CAPLUS
DN 111:94012
TI Preliminary study of the inheritance of temperature ***stress*** proteins in barley (Hordeum vulgare L.)
AU Marmiroli, Nelson; Lorenzoni, Carlo; Stanca, A. Michele; Terzi, Valeria
CS Inst. Genet., Univ. Lecce, Lecce, 73100, Italy
SO Plant Science (Shannon, Ireland) (1989), 62(2), 147-56
CODEN: PLSCE4; ISSN: 0168-9452
DT Journal
LA English
AB Comparisons of 3 barley genotypes, 2 parentals and their F1 offspring, were made for protein synthesis modifications upon exposure to a wide range of temps. from 5 to 40.degree.. The 2 parental genotypes were ***selected*** for their differences in growth habit, geog. origin, spike type and cold hardiness characteristics. Moreover, the 2 genotypes differed in specific proteins which appeared at low or at high temps. The F1 progeny obtained showed the following characteristics: (1) some of the heat ***stress*** induced proteins (HSP) had similarity with those of the parentals; the highest no. of similarities was found between F1 and the Georgie parental; (2) the pattern of HSP induced was different at 34 and 40.degree., a temp. dependency which is typical of Onice at the level of coleoptiles and specific of Georgie at the level of roots; and (3) a relevant no. of HSP in F1 had no parental counterparts, i.e. they were F1 or hybrid specific. Anal. of the cold induced proteins (CSP) showed the F1 progeny inherited most of the CSP characteristics of both parentals, though with a preference of the Onice parental at least at the level of coleoptiles. These results, that few ***stress*** ***genes*** had an uniparental heredity, whereas other ***stress*** ***genes*** showed an F1 specific pattern of expression, may probably be a consequence of new ***regulatory*** interactions which took place in the hybrid between the ***stress*** ***genes*** of the 2 parentals.

L7 ANSWER 79 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1987:593009 CAPLUS
DN 107:193009
TI Agricultural-chemical-producing endosymbiotic microorganisms and method for preparing and using them
IN Carlson, Peter S.
PA Crop Genetics International N. V., USA
SO PCT Int. Appl., 98 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
---------- ---- -------- ---------- --------
PI WO 8703303 A1 19870604 WO 1986-US2494 19861119 W: AU, JP RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE AU 8767232 A1 19870701 AU 1987-67232 19861119 AU 610490 B2 19910523 EP 245489 A1 19871119 EP 1986-907205 19861119 EP 245489 B1 19940330 R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE JP 01502475 T2 19890831 JP 1986-506373 19861119 EP 583675 A1 19940223 EP 1993-112393 19861119 R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE AT 103634 E 19940415 AT 1986-907205 19861119 ZA 8608798 A 19880727 ZA 1986-8798 19861120
PRAI US 1985-799999 19851120 EP 1986-907205 19861119 WO 1986-US2494 19861119
AB Hybrid agrochem.-producing microorganisms capable of entering into end osymbiotic relationship with ***plants*** , while not causing diseases, are produced by fusion of genetic material from the producer microorganism and a ***plant*** -infecting microorganism. Polyethylene glycol 6000 facilitated protoplast fusion of N-fixation competent Azobacter vinelandii with Erwinia stewartii was performed and the mixt. grown and ***selected*** in Burke's N-free medium contg. antibiotics. The mixed fusion hybrids were injected to corn seedlings to allow the fusion bacteria interact with corn cells and spread. The fusion hybrid bacteria were recovered from the corn tissue, grown and formed colonies in Burke's N-free medium, and the ***selected*** colonies were back injected into the corn to further ***select*** the hybrids which gave the most vigorous growth while not causing diseases. The corn injected with the ***selected*** hybrids grown in N- ***stressed*** condition produced 29-108% greater yield than the control.

L7 ANSWER 80 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1987:530413 CAPLUS
DN 107:130413
TI Object identification and measurement from images with access to the database to ***select*** specific subpopulations of special interest
AU Rutherford, H. G.; Taub, F. E.; Williams, B.
CS TAU Corp., Los Gatos, CA, 95030, USA
SO Proceedings of SPIE-The International Society for Optical Engineering (1987), 757(Methods Handl. Process. Imagery), 40-7 CODEN: PSISDG; ISSN: 0277-786X
DT Journal
LA English
AB An automated vision image anal. system to analyze images resulting from nucleic acid hybridizations is presented. Real-time image acqusition from autoradiographs is accomplished with a sensitivity to optical d. to the degree that any spot visible by eye can be quantified by digital methods and enhanced by image processing techniques for observation. The system provides a tool for quantification of differences in ***gene*** expression, rapid processing of thousands of pairs of ***genes*** , storage in a database, search for small differences, large differences, and infrequently occurring ***genes*** . Background correction, normalization, and pseudocolor mapping facilitate comparison and quantification directly from the CRT display. The image pairs, a percent change image and a difference image are presented in a quad display with coordinated spot d. and change measurement simultaneously for each of the four images. The system provides a tool for anal. of altered ***gene*** expression in response to environmental ***stress*** , such as heat-shock and salt water in ***plant*** growth; hormone ***regulation*** , such as before and after hormone administration in animals; development; and carcinogenesis. The use of this system to study nucleic acid hybridization is contrasted with the study of 2-D protein electrophoresis gels

for the detn. of changes in ***gene*** expression and identification of corresponding proteins of significance.

L7 ANSWER 81 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1987:471934 CAPLUS
DN 107:71934
TI Chalcone isomerase cDNA cloning and mRNA induction by fungal elicitor, wounding and infection
AU Mehdy, Mona C.; Lamb, Christopher J.
CS Plant Biol. Lab., Salk Inst. Biol. Stud., San Diego, CA, 92138, USA
SO EMBO Journal (1987), 6(6), 1527-33 CODEN: EMJODG; ISSN: 0261-4189
DT Journal
LA English
AB The environmentally ***regulated*** synthesis of phenylpropanoid natural products was studied by examg. the expression of the ***gene*** encoding chalcone isomerase (CHI). This enzyme catalyzes a step common to the synthesis of flavonoid pigments and isoflavonoid phytoalexins. A .lambda.g11 library was constructed using mRNA from cell cultures of bean (Phaseolus vulgaris) treated with fungal elicitor. Two pos. clones were obtained by screening 105 recombinants with an antiserum to purified bean CHI. The identity of the cloned sequences was confirmed by hybrid-***select*** translation and the prodn. of antigenic polypeptides from transcripts synthesized in vitro. Addn. of elicitor to cell cultures resulted in the rapid accumulation of CHI mRNA, with max. levels achieved 3-4 h after elicitation. CHI mRNA also accumulated during the natural infection of hypocotyls with the fungal pathogen Colletotrichum lindemuthianum, and in mech. wounded hypocotyls. The kinetics of accumulation of CHI mRNA in response to these environmental signals were strikingly similar to those of mRNAs encoding 2 other phenylpropanoid pathway enzymes, phenylalanine ammonialyase and chalcone synthase. In contrast to the multi- ***gene*** families encoding these 2 enzymes, chalcone isomerase is encoded by a single ***gene*** which is ***regulated*** by several environmental stimuli.

L7 ANSWER 82 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1987:436159 CAPLUS
DN 107:36159
TI Somatic embryogenesis and ***plant*** regeneration in cotton (Gossypium hirsutum L.)
AU Trolinder, Norma L.; Goodin, J. R.
CS Dep. Biol. Sci., Texas Tech Univ., Lubbock, TX, 79409, USA
SO Plant Cell Reports (1987), 6(3), 231-4 CODEN: PCRPD8; ISSN: 0721-7714
DT Journal
LA English
AB A method for regeneration of cotton which includes a morphogenetically competent cell suspension was needed to facilitate ***selection*** of ***stress*** -resistant variants and ***gene*** manipulation. Preliminary screening of 8 strains of Gossypium hirsutum for embryogenic potential resulted in the prodn. of somatic embryos in all strains. Coker 312 was ***selected*** for use in the development of a model regeneration system for G. hirsutum. Calli were initiated from hypocotyl tissues of 3-day-old-seedlings. Globular embryos were present after 6 wk in culture. Calli were subcultured to liq. suspension in growth ***regulator*** -free medium. After 3-4 wk, suspensions were sieved to collect globular and heart stage embryos. Collected embryos developed further when plated onto semisolid medium. To induce germination and ***plantlet*** growth, mature embryos were placed on sterile vermiculite satd. with medium. Upon development of roots and 2 true levels, ***plantlets*** were potted in peat and sand, and hardened. Mature ***plants*** and progeny were obtained with this procedure. A high percentage of infertile ***plants*** was obsd. among the regenerants.

L7 ANSWER 83 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1987:401838 CAPLUS
DN 107:1838
TI ***Regulation*** of the transcription of heat shock ***genes*** in nuclei from soybean (Glycine max) seedlings
AU Schoeffl, F.; Rossol, I.; Angermueller, S.
CS Fak. Biol., Univ. Bielefeld, Bielefeld, 4800/1, Fed. Rep. Ger.
SO Plant, Cell and Environment (1987), 10(2), 113-19 CODEN: PLCEDV; ISSN: 0140-7791
DT Journal
LA English
AB Run-off transcription in nuclei isolated from soybean seedlings was used to test the hypothesis that the expression heat shock ***genes*** is controlled at the level of transcription. Only nuclei pretreated by a heat shock at 41.degree. prior to their isolation synthesized RNA from heat shock ***genes*** . The specificity of transcripts was detd. by Southern blot hybridization of [32P]-labeled run-off RNA with DNA fragments from several heat shock and non-heat shock ***genes*** . The strand ***selectivity*** of heat shock ***gene*** transcription was exemplified by single stranded DNA probes. Low concns. of .alpha.-amanitin completely inhibited the synthesis of heat shock specific RNA, but only partially inhibited the synthesis of rRNA. The overall transcription of nuclei isolated from heat shock tissue was reduced by more than 20% compared to that in nuclei from control tissue. This decline is consistent with a decrease in the transcriptional activity of nonheat shock ***genes*** transcribed by RNA polymerase I and II. The results suggest that temp. ***stress*** induces the transcriptional activation of heat shock ***genes*** and has a neg. effect on the transcription of other ***genes*** .

L7 ANSWER 84 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1986:622947 CAPLUS
DN 105:222947
TI Examples of the use of natural and synthetic ***plant*** growth substances in cereal breeding
AU Quarrie, S. A.; Gale, M. D.
CS Plant Breed. Inst., Trumpington/Cambridge, CB2 2LQ, UK
SO Plant Growth Subst. 1985, Proc. Int. Conf., 12th (1986), Meeting Date 1985, 404-9. Editor(s): Bopp, Martin. Publisher: Springer, Berlin, Fed. Rep. Ger. CODEN: 55GUAK
DT Conference
LA English
AB Gibberellin-insensitivity in wheat in the form of the Rht1 and Rht2 dwarfing ***genes*** not only reduced height, but also confered a consistent and significant yield advantage in the range of genetic background and with different water regimes. High-ABA lines had higher water use efficiencies than low-ABA lines; this was assocd. with significantly higher yields (5-6%).

L7 ANSWER 85 OF 85 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1986:201587 CAPLUS
DN 104:201587
TI Eukaryotic hybrid vectors and preparation of polypeptides
IN Hinnen, Albert; Kuenzler, Peter
PA Ciba-Geigy A.-G., Switz.
SO PCT Int. Appl., 81 pp. CODEN: PIXXD2

DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 8600089 A1 19860103 WO 1985-EP278 19850611 W: DK, JP, US RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE EP 182838 A1 19860604 EP 1985-902543 19850611 R: AT, BE, CH, DE, FR, GB, IT, LI, NL, SE JP 61502377 T2 19861023 JP 1985-502588 19850611 DK 8600704 A 19860213 DK 1986-704 19860213 IL 84702 A1 19930708 IL 1987-84702 19871203
PRAI GB 1984-15186 19840614 WO 1985-EP278 19850611
AB Polypeptides can be formed by genetically engineered eukaryotic cells with extrachromosomal rRNA-specifying DNA (rDNA) used as a cloning vector for introducing the foreign ***gene*** into these eukaryotic cells. The eukaryotic hybrid cloning vectors contain extrachromosomal rDNA from organisms such as Dictyostelium discoideum, Tetrahymena, Paramecium, Oxytrichia, stylorichia, or Physarum polycephalum. For example, in P. polycephalum, the rDNA is obtained following extrachromosomal DNA digestion with BglII restriction endonuclease. The eukaryotic hybrid cloning vectors contain both the PHO5 promoter and PHO5 transcription termination signals and the foreign ***gene*** to be cloned. These ***genes*** can code for a polypeptide hormone, an immunomodulatory polypeptide, an anti-viral or anti-tumor polypeptide, an antibody, viral antigen, vaccine, blood clotting factor, ***plant*** pest-resistance factor, heat-resistance factor, desiccation-resistance factor, ***plant*** growth factor, or human tissue plasminogen activator. Suitable host organisms for these cloning vectors include yeast such as Saccharomyces cerevisiae, ***plant*** cells (e.g. Nicotiana tabacum), invertebrates, and vertebrate cells. Some eukaryotic cells having cell walls are 1st converted to spheroplasts or protoplasts, treated with the eukaryotic hybrid vector using the Ca phosphate pptn. method, and the cell wall regenerated prior to ***selection*** .

=> d his
(FILE 'HOME' ENTERED AT 16:01:54 ON 26 FEB 2004)
FILE 'CAPLUS' ENTERED AT 16:02:05 ON 26 FEB 2004
L1 592 S (PLANT? AND STRESS? AND SELECT? AND GENE#)/BI,AB
L2 205 S L1 AND REGULAT?/BI,AB
L3 200 S L2 NOT 2004/PY
L4 161 S L3 NOT 2003/PY
L5 117 S L4 NOT 2002/PY
L6 96 S L5 NOT 2001/PY

L7 85 S L6 NOT 2000/PY

=> s l5 not l7

L8 32 L5 NOT L7

=> d l8 1-32 bib ab

L8 ANSWER 1 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:460883 CAPLUS
DN 137:212733
TI In silico characterization and expression analyses of sugarcane putative sucrose non-fermenting-1 (SNF1) related kinases
AU Carraro, Dirce Maria; Lambais, Marcio R.; Carrer, Helaine
CS Ludwig Institute for Cancer Research, Sao Paulo, 01509-010, Brazil
SO Genetics and Molecular Biology (2001), 24(1-4), 35-41
CODEN: GMBIFG; ISSN: 1415-4757
PB Sociedade Brasileira de Genetica
DT Journal
LA English
AB Sucrose non-fermenting-1-related protein kinases (SnRKs) may play a major role in ***regulating*** ***gene*** expression in ***plant*** cells. This family of ***regulatory*** proteins is represented by sucrose non-fermenting-1 (SNF1) protein kinase in Saccharomyces cerevisiae, AMP-activated protein kinases (AMPKs) in mammals and SnRKs in higher ***plants*** . The SnRK family has been reorganized into three subfamilies according to the evolutionary relationships of their amino acid sequences. Members of the SnRK subfamily have been identified in several ***plants*** . There is evidence that they are involved in the nutritional and/or environmental ***stress*** response, although their roles are not yet well understood. We have identified at least 22 sugarcane expressed sequence tag (EST) contigs encoding putative SnRKs. The amino acid sequence alignment of both putative sugarcane SnRKs and known SnRKs revealed a highly conserved N-terminal catalytic domain. Our results indicated that sugarcane has at least one member of each SnRK subfamily. Expression pattern anal. of sugarcane EST-contigs encoding putative SnRKs in 26 ***selected*** cDNA libraries from the sugarcane expressed sequence tag SUCEST database has indicated that members of this family are expressed throughout the ***plant*** . Members of the same subfamily showed no specific expression patterns, suggesting that their functions are not related to their phylogenic relationships based on N-terminal amino acid sequence phylogenetic relationships.
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 2 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:395441 CAPLUS
DN 136:366544
TI ***Genes*** expressed during early stages of rice infection with the rice blast fungus Magnaporthe grisea
AU Rauyaree, Payungsak; Choi, Woobong; Fang, Eric; Blackmon, Barbara; Dean, Ralph A.
CS Department of Plant Pathology and Physiology, Clemson University, Clemson, SC, 29634, USA
SO Molecular Plant Pathology (2001), 2(6), 347-354 CODEN: MPPAFD; ISSN: 1464-6722
PB Blackwell Science Ltd.
DT Journal
LA English
AB A system-wide approach was adopted to further elucidate mechanisms ***regulating*** disease outcome between rice and the fungal pathogen Magnaporthe grisea. First, a cDNA library was constructed from M. grisea infected rice at 48 h post-inoculation. The 5' end-sequencing of 619 randomly ***selected*** clones revealed 359 expressed sequence tags (ESTs) that had not previously been described. A total of 124 from 260 ESTs with high and moderate similarity scores, based on BLASTX, were organized into categories according to their putative function. The largest category of sequences (21%) contained ***stress*** or defense response ***genes*** . Eleven percent of identified ESTs were redundant. In a second approach, differential hybridization anal. of the cDNA library using high-d. filters resulted in the identification of novel ***genes*** and previously characterized M. grisea ***genes*** , including several that

had previously been implicated in the infection process. A survey of up- ***regulated*** cDNA clones revealed clone 29003, which corresponded to the rice peroxidase POX22.3. This ***gene*** is known to be expressed in rice upon infection with Xanthomonas oryzae pv. oryzae, the bacterial blight pathogen. Importantly, this approach demonstrates the utility of ***gene*** discovery, through ESTs, for revealing novel ***genes*** in addn. to those previously characterized as being potentially implicated in host-pathogen interactions. The EST sequences are deposited in GenBank under Accession Nos. AW154962-AW155632 and AW069892-AW070183.
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 3 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:217671 CAPLUS
DN 136:364450
TI Introduction of ***genes*** encoding C4 photosynthesis enzymes into rice ***plants*** : physiological consequences
AU Ku, Maurice S. B.; Cho, Dongha; Li, Xia; Jiao, De-Mao; Pinto, Manuel; Miyao, Mitsue; Matsuoka, Makoto
CS School of Biological Sciences, Washington State University, Pullman, WA, 99164-4236, USA
SO Novartis Foundation Symposium (2001), 236(Rice Biotechnology), 100-116 CODEN: NFSYF7; ISSN: 1528-2511
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB Transgenic rice ***plants*** expressing the maize phosphoenolpyruvate carboxylase (PEPC) and pyruvate, orthophosphate dikinase (PPDK) exhibit a higher photosynthetic capacity (up to 35%) than untransformed ***plants*** . The increased photosynthetic capacity in these ***plants*** is mainly assocd. with an enhanced stomatal conductance and a higher internal CO2 concn. ***Plants*** simultaneously expressing high levels of both enzymes also have a higher photosynthetic capacity. The results suggest that both PEPC and PPDK play a key role in org. acid metab. in the guard cells to ***regulate*** stomatal opening. Under photoinhibitory and photooxidative conditions, PEPC transgenic rice ***plants*** are capable of maintaining a higher photosynthetic rate, a higher photosynthetic quantum yield by PSII and a higher capacity to dissipate excess energy photochem. and non-photochem. than untransformed ***plants*** . Preliminary data from field trials show that relative to untransformed ***plants*** , the grain yield is about 10-20% higher in ***selected*** PEPC and 30-35% higher in PPDK transgenic rice ***plants*** , due to increased tiller no. Taken together, these results suggest that introduction of C4 photosynthesis enzymes into rice has a good potential to enhance its tolerance to ***stress*** , photosynthetic capacity and yield.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 4 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:90973 CAPLUS
DN 136:276240
TI The transcripts of several components of the protein synthesis machinery are cold- ***regulated*** in a chloroplast-dependent manner in barley and wheat
AU Baldi, Paolo; Vale, Giampiero; Mazzucotelli, Elisabetta; Govoni, Chiara; Faccioli, Primetta; Stanca, A. Michele; Cattivelli, Luigi
CS Experimental Institute for Cereal Research, Fiorenzuola d'Arda, I-29017, Italy
SO Journal of Plant Physiology (2001), 158(12), 1541-1546
CODEN: JPPHEY; ISSN: 0176-1617
PB Urban & Fischer Verlag
DT Journal
LA English
AB Nine clones coding different components of the protein synthesis machinery were ***selected*** from an EST barley library prepd. from cold exposed ***plants*** and tested for their expression at low temp. Northern anal. revealed that expression of elongation factor (EF) 1B.beta. and two ribosomal protein (RP) ***genes*** S7 and L7A was enhanced following exposure to 3.degree.C, but not during dehydration or exogenous ABA treatment. The mRNA levels of EF1B.beta., RPS7, and RPL7A did not vary between cultivars with different frost tolerance, but differences in expression were found between different species. Expts. with an albino mutant and etiolated ***plants*** revealed that the cold-dependent ***regulation*** of EF1B.beta., RPS7, and RPL7A transcripts is controlled by a chloroplast-related pathway impaired in the mutant.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 5 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:53409 CAPLUS
DN 136:244357
TI Genetic bases of salt and cold tolerance in tomato and the prospect for developing tolerant cultivars
AU Foolad, Majid R.
CS Department of Horticulture, The Pennsylvania State University, University Park, PA, 16802, USA
SO Current Topics in Plant Biology (2000), 2, 35-49 CODEN: CTPBF2
PB Research Trends
DT Journal; General Review
LA English
AB A review. ***Plant*** response to environmental ***stress*** is complex; it is controlled by more than one ***gene*** and highly affected by other environmental variables, typical of quant. traits. In addn., ***stress*** response is a developmentally ***regulated*** , stage specific phenomenon. Tolerance at one stage of ***plant*** development is often not correlated with tolerance at other developmental stages. Specific ontogenic stages, including seed germination and emergence, seedling survival and growth, and vegetative growth and reprodn., should be evaluated sep. for assessment of tolerance and identification, characterization and genetic manipulation of tolerance components. We have investigated genetic controls of salt tolerance (ST) and cold tolerance (CT) during seed germination and vegetative growth in tomato, using conventional protocols of ***plant*** genetics and breeding and contemporary techniques of mol. markers and quant. trait loci (QTLs) anal. The overall results have indicated that, unlike the traditional viewpoint that quant. traits are controlled by many small-effect ***genes*** (QTLs) whose individual effects can not be detd., ST or CT at each ***plant*** stage is generally controlled by a few QTLs with major effects and several QTLs with smaller effects. The major QTLs can be further characterized genetically for map-based cloning of ***stress*** tolerance ***genes*** and for use in marker-assisted breeding for ***stress*** tolerance. The results have also indicated that different QTLs affect ***stress*** tolerance at different developmental stages and that

selection for tolerance at one stage does not affect tolerance at other stages. However, the identification of QTLs for tolerance at different stages should facilitate simultaneous or sequential introgression of QTLs to develop genotypes with enhanced tolerance at more than one stage. For the seed germination stage, two types of QTLs were identified: ***stress*** -nonspecific QTLs which affected germination rate under both ***stress*** and nonstress conditions, and ***stress*** -specific QTLs, which affected germination only under salt- ***stress*** or cold- ***stress*** but not nonstress conditions. In comparison, no genetic relationship was obsd. between ***plant*** ST and CT during vegetative growth. Despite the apparent complexities of genetic controls of ST and CT in tomato, the current knowledge indicates a good prospect for improving these traits in com. tomato cultivars via marker-assisted breeding.
RE.CNT 95 THERE ARE 95 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 6 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:49074 CAPLUS
DN 137:42382
TI Molecular characterization of XVT8, a ***stress*** -responsive ***gene*** from the resurrection ***plant*** Xerophyta viscosa Baker
AU Ndima, Tozama; Farrant, Jill; Thomson, Jennifer; Mundree, Sagadevan
CS Microbiology Department, University of Cape Town, Rondebosch, S. Afr.
SO Plant Growth Regulation (2001), 35(2), 137-145 CODEN: PGRED3; ISSN: 0167-6903
PB Kluwer Academic Publishers
DT Journal
LA English
AB Xerophyta viscosa (Baker) is a monocotyledonous resurrection ***plant*** that is capable of tolerating extremes of desiccation. Upon rewatering, it rehydrates completely, assuming its full physiol. activities. Studies on changes in ***gene*** expression assocd. with dehydration ***stress*** tolerance were conducted. A cDNA library was constructed from mRNA isolated from dehydrated X. viscosa leaves [85%, 37% and 5% relative water content (RWC)]. XVT8 represents one of 30 randomly ***selected*** clones that were differentially expressed when X. viscosa was dehydrated. Sequence anal. of XVT8 revealed that XVT8 exhibited 45% and 43% identity to dehydrin proteins from Arabidopsis thaliana and Pisum sativum resp., at the amino acid level. XVT8 encodes a glycine-rich protein (27 kDa) which is largely hydrophilic and contains a hydrophobic segment at the C-terminus. Southern blot anal. confirmed the presence of XVT8 in the X. viscosa genome. XVT8 transcripts accumulated in X. viscosa ***plants*** that were exposed to heat, low temp. and dehydration ***stresses*** , and to exogenous abscisic acid and ethylene. These results provide direct evidence for the heat, low temp., dehydration, abscisic acid and ethylene-dependent ***regulation*** of the XVT8 ***gene*** in X. viscosa.
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 7 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:889731 CAPLUS
DN 136:162234
TI In vivo target promoter-binding activities of a xenobiotic ***stress*** -activated TGA factor
AU Johnson, Christopher; Boden, Erin; Desai, Mihir; Pascuzzi, Pete; Arias, Jonathan
CS Center for Agricultural Biotechnology, University of Maryland Biotechnology Institute, College Park, MD, 20742, USA
SO Plant Journal (2001), 28(2), 237-243 CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Science Ltd.
DT Journal
LA English
AB Xenobiotic chems. induce the expression of nuclear detoxification ***genes*** . A full understanding of this protective response will require characterization of its transcriptional ***regulatory*** machinery. We describe here the use of a recently developed ***plant*** chromatin immunopptn. (ChIP) assay to define nuclear promoter targets of TGA1a, a tobacco basic/leucine zipper transcription factor whose activity is potentiated by herbicide-induced xenobiotic ***stress*** . TGA1a ***selectively*** binds as-1-type cis-elements, which ***regulate*** transcription of putative detoxification and defense ***genes*** . With ChIP, we show that endogenous TGA1a binds as-1-contg. promoter sequences of two tobacco glutathione S-transferase ***genes*** , GNT1 and GNT35. This binding activity is strongly enhanced by xenobiotic ***stress*** , as is expression of these ***genes*** . In contrast, TGA1a apparently does not bind in vivo to functional as-1 elements in promoters of PR-1a and PG13, ***genes*** whose expression is insensitive to this stimulus. The findings here thus discriminate between a no. of possible functional promoter binding sites for a trans- ***regulatory*** factor, within the context of a signal response pathway.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 8 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:694874 CAPLUS
DN 136:242687
TI Nitrate-induced ***genes*** in tomato roots. Array analysis reveals novel ***genes*** that may play a role in nitrogen nutrition
AU Wang, Yi-Hong; Garvin, David F.; Kochian, Leon V.
CS United States Plant, Soil, Laboratory, United States Department of Agriculture-Agricultural Research Service, Cornell University, Ithaca, NY, 14853, USA
SO Plant Physiology (2001), 127(1), 345-359 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Biologists
DT Journal
LA English
AB A subtractive tomato (Lycopersicon esculentum) root cDNA library enriched in ***genes*** up- ***regulated*** by changes in ***plant*** mineral status was screened with labeled mRNA from roots of both nitrate-induced and mineral nutrient-deficient (-nitrogen [N], -phosphorus, -potassium [K], -sulfur, -magnesium, -calcium, -iron, -zinc, and -copper) tomato ***plants*** . A subset of cDNAs was ***selected*** from this library based on mineral nutrient-related changes in expression. Addnl. cDNAs were ***selected*** from a second mineral-deficient tomato root library based on sequence homol. to known ***genes*** . These ***selection*** processes yielded a set of 1,280 mineral nutrition-related cDNAs that were arrayed on nylon membranes for further anal. These high-d. arrays were hybridized with mRNA from tomato ***plants*** exposed to nitrate at different time points after N was withheld for 48 h, for ***plants*** that

were grown on nitrate/ammonium for 5 wk prior to the withholding of N. One hundred-fifteen ***genes*** were found to be up- ***regulated*** by nitrate resupply. Among these ***genes*** were several previously identified as nitrate responsive, including nitrate transporters, nitrate and nitrite reductase, and metabolic enzymes such as transaldolase, transketolase, malate dehydrogenase, asparagine synthetase, and histidine decarboxylase. We also identified 14 novel nitrate-inducible ***genes*** , including: (a) water channels, (b) root phosphate and K+ transporters, (c) ***genes*** potentially involved in transcriptional ***regulation*** , (d) ***stress*** response ***genes*** , and (e) ribosomal protein ***genes*** . In addn., both families of nitrate transporters were also found to be inducible by phosphate, K, and iron deficiencies. The identification of these novel nitrate-inducible ***genes*** is providing avenues of research that will yield new insights into the mol. basis of ***plant*** N nutrition, as well as possible networking between the ***regulation*** of N, phosphorus, and K nutrition.
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 9 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:694856 CAPLUS
DN 135:367540
TI ***Regulation*** of the Arabidopsis transcriptome by oxidative ***stress***
AU Desikan, Radhika; A.-H.-Mackerness, Soheila; Hancock, John T.; Neill, Steven J.
CS Centre for Research in Plant Science, University of the West of England, Bristol, Bristol, BS16 1QY, UK
SO Plant Physiology (2001), 127(1), 159-172 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Biologists
DT Journal
LA English
AB Oxidative ***stress*** , resulting from an imbalance in the accumulation and removal of reactive oxygen species such as hydrogen peroxide (H2O2), is a challenge faced by all aerobic organisms. In ***plants*** , exposure to various abiotic and biotic ***stresses*** results in accumulation of H2O2 and oxidative ***stress*** . Increasing evidence indicates that H2O2 functions as a ***stress*** signal in ***plants*** , mediating adaptive responses to various ***stresses*** . To analyze cellular responses to H2O2, we have undertaken a large-scale anal. of the Arabidopsis transcriptome during oxidative ***stress*** . Using cDNA microarray technol., we identified 175 non-redundant expressed sequence tags that are ***regulated*** by H2O2. Of these, 113 are induced and 62 are repressed by H2O2. A substantial proportion of these expressed sequence tags have predicted functions in cell rescue and defense processes. RNA-blot analyses of ***selected*** ***genes*** were used to verify the microarray data and extend them to demonstrate that other ***stresses*** such as wilting, UV irradn., and elicitor challenge also induce the expression of many of these ***genes*** , both independently of, and, in some cases, via H2O2.
RE.CNT 86 THERE ARE 86 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 10 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:678340 CAPLUS
DN 136:34655
TI Epigenetic modifications in maize parental inbreds and hybrids and their relationship to hybrid vigor and stability
AU Tsaftaris, Athanasios S.; Polidoros, Alexios N.; Tani, Eleni
CS Department of Genetics and Plant Breeding, Aristotelian University of Thessaloniki, Thessaloniki, 54006, Greece
SO Gene Families: Studies of DNA, RNA, Enzymes and Proteins, Proceedings of the International Congress on Isozymes, 10th, Beijing, China, Oct. 5-10, 1999 (2001), Meeting Date 1999, 277-286. Editor(s): Xue, Guoxiong. Publisher: World Scientific Publishing Co. Pte. Ltd., Singapore, Singapore. CODEN: 69BUWM
DT Conference; General Review
LA English
AB A review. DNA methylation is an epigenetic genome-wide general ***regulatory*** mechanism that affects qual. and quant. the expression of many ***genes*** and has been considered important for the manifestation of heterosis. DNA methylation in maize was found to be genotype, tissue and developmental stage specific. Growth conditions affected the level and pattern of DNA methylation. Our studies indicated that hybrids were less methylated than their parental inbreds and remained less methylated under ***stress*** . These findings support the hypothesis that ***selection*** of inbreds may lead to gradual accumulation of methylated sites, which could be released and/or re-patterned when the lines are crossed to generate hybrids.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 11 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:660921 CAPLUS
DN 136:3059
TI Development and characterization of an adapted form of droopy, a diploid potato mutant deficient in abscisic acid
AU De Jong, H.; Kawchuk, L. M.; Coleman, W. K.; Verhaeghe, C. A.; Russell, L.; Burns, V. J.; Tremblay-Deveau, E.
CS Potato Research Centre, Agriculture and Agri-Food Canada, Fredericton, NB, E3B 4Z7, Can.
SO American Journal of Potato Research (2001), 78(4), 279-290 CODEN: AJPRFQ; ISSN: 1099-209X
PB Potato Association of America
DT Journal
LA English
AB A cultivated diploid potato breeding population has been ***selected*** for adaptation to growing, tuberizing (under relatively long days), and storing (including long dormancy) under New Brunswick conditions. In this population, a mutant was discovered that appeared similar to the earlier described droopy mutant, which is deficient in abscisic acid and is unable to ***regulate*** water loss from its leaves. The physiol. and genetics of the newly discovered mutant were studied and compared in detail with the description of droopy. This mutant has a longer tuber dormancy than the original droopy. In families segregating for droopy and normal, similar dormancies and endogenous abscisic acid levels in tubers were obsd. between droopy and normal genotypes. The effect of the mutant ***gene*** appears to be tissue specific, affecting aboveground ***plant*** parts only. A test for allelism indicated that this mutant is allelic to droopy. Classical linkage analyses confirmed previously reported close linkage between the Dr (droopy) and the S (incompatibility) loci. The Dr locus has been mapped in this study to the top of chromosome I. Several test crosses indicated reciprocal differences in the segregation rations between droopy and normal. In keeping with the droopy (drdr) genotype, drought-***stressed*** leaves of the mutant were incapable of

increasing abscisic acid prodn. compared to the normal. This mutant, with its apparent developmentally restricted expression, may be useful in elucidating the genetic and physiol. processes assocd. with such major events as tuberization, response to drought ***stress*** and tuber dormancy.
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 12 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:660244 CAPLUS
DN 136:306753
TI Molecular analysis of differentially expressed ***genes*** during postharvest deterioration in cassava (Manihot esculenta Crantz) tuberous roots
AU Huang, Jiang; Bachem, Christian; Jacobsen, Evert; Visser, Richard G. F.
CS Laboratory of Plant Breeding, Department of Plant Sciences, The Graduate School of Experimental Plant Science (EPS), Wageningen University, Wageningen, 6700 AJ, Neth.
SO Euphytica (2001), 120(1), 85-93 CODEN: EUPHAA; ISSN: 0014-2336
PB Kluwer Academic Publishers
DT Journal
LA English
AB One of the major problems for cassava is the rapid deterioration after harvesting cassava tuberous roots, which limits the possibilities for prodn. and distribution of cassava in the world. Postharvest deterioration is an inherent problem for cassava since wounding and mech. damage of the tuberous roots cannot be prevented during harvesting, which includes postharvest physiol. deterioration (PPD) and secondary deterioration. To date, the mol. mechanism and biochem. pathways of PPD are poorly understood. The aim of this project, which is focusing on the early stages (first 72 h), is to gain mol. insight and identify important metabolic pathways during the process of PPD in cassava tuberous roots. Finally by reverse genetic approaches to delay or even prevent the process of PPD in cassava tuberous roots. By using a new RNA fingerprinting method, called cDNA-AFLP, we have screened more than 6000 TDFs (Transcript Derived Fragments) via up to 100 primer combinations during the early process of PPD in cassava. Only 10% of the TDFs are developmentally ***regulated*** , while the other 90% are expressed throughout the process of PPD in cassava tuberous roots. Furthermore, in order to set up a functional catalog of differentially expressed ***genes*** during PPD, 70 TDFs were ***selected*** and isolated based on their expression patterns, which were either up- ***regulated*** , down-***regulated*** or transiently induced. Around 40 of these TDFs were found to be similar with known ***genes*** in databases. The other 30 TDFs were present mostly ***genes*** without known function. Through data anal., it is shown that important biochem. and physiol. processes, such as notably oxygen ***stress*** , carbohydrate metab., protein metab. and phenolic compds. synthesis, are involved in PPD in cassava tuberous roots.
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 13 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:647424 CAPLUS
DN 136:319258
TI St John's wort, hypericin, and imipramine: a comparative analysis of mRNA levels in brain areas involved in HPA axis control following short-term and long-term administration in normal and ***stressed*** rats
AU Butterweck, V.; Winterhoff, H.; Herkenham, M.
CS Institute of Pharmacology and Toxicology, Muenster, 48149, Germany
SO Molecular Psychiatry (2001), 6(5), 547-564 CODEN: MOPSFQ; ISSN: 1359-4184
PB Nature Publishing Group
DT Journal
LA English
AB Clin. studies demonstrate that the antidepressant efficacy of St John's wort (Hypericum) is comparable to that of tricyclic antidepressants such as imipramine. Onset of efficacy of these drugs occurs after several weeks of treatment. Therefore, we used in situ hybridization histochem. to examine in rats the effects of short-term (2 wk) and long-term (8 wk) administration of imipramine, Hypericum ext., and hypericin (an active constituent of St John's wort) on the expression of ***genes*** that may be involved in the ***regulation*** of the hypothalamic-pituitary- adrenal (HPA) axis. Imipramine (15 mg kg-1), Hypericum (500 mg kg-1), and hypericin (0.2 mg kg-1) given daily by gavage for 8 wk but not for 2 wk significantly decreased levels of corticotropin-releasing hormone (CRH) mRNA by 16-22% in the hypothalamic paraventricular nucleus (PVN) and serotonin 5-HT1A receptor mRNA by 11-17% in the hippocampus. Only imipramine decreased tyrosine hydroxylase (TH) mRNA levels in the locus coeruleus (by 23%), and only at 8 wk. The similar delayed effects of the three compds. on ***gene*** transcription suggests a shared action on the centers that control HPA axis activity. A second study was performed to assess the effects of long-term imipramine and Hypericum administration on ***stress*** -induced changes in ***gene*** transcription in ***stress*** -responsive circuits. Repeated immobilization ***stress*** (2 h daily for 7 days) increased mRNA levels of CRH in the PVN, proopiomelanocortin (POMC) in the anterior pituitary, glutamic acid decarboxylase (GAD 65/67) in the bed nucleus of the stria terminalis (BST), cAMP response element binding protein (CREB) in the hippocampus, and TH in the locus coeruleus. It decreased mRNA levels of 5-HT1A and brain-derived neurotrophic factor (BDNF) in the hippocampus. Long-term pretreatment with either imipramine or Hypericum reduced to control levels the ***stress*** -induced increases in ***gene*** transcription of GAD in the BST, CREB in the hippocampus, and POMC in the pituitary. The ***stress*** -induced increases in mRNA levels of CRH in the PVN and TH in the locus coeruleus were reduced by imipramine but not by Hypericum. The ***stress*** -induced decreases in BDNF and 5-HT1A mRNA levels were not prevented by either drug. Taken together, these data show: (1) that Hypericum and hypericin have delayed effects on HPA axis control centers similar to those of imipramine; and (2) that ***select*** ***stress*** -induced changes in ***gene*** transcription in particular brain areas can be prevented by long-term treatment with either the prototypic tricyclic antidepressant imipramine or the herbiceutical St John's wort. However, imipramine appears to be more effective in blocking ***stress*** effects on the HPA axis than the ***plant*** ext.
RE.CNT 79 THERE ARE 79 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 14 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:561198 CAPLUS
DN 135:270108

TI Metabolic engineering of essential oil yield and composition in mint by altering expression of deoxyxylulose phosphate reductoisomerase and menthofuran synthase
AU Mahmoud, Soheil S.; Croteau, Rodney B.
CS Institute of Biological Chemistry, Washington State University, Pullman, WA, 99164-6340, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2001), 98(15), 8915-8920 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Peppermint (Mentha .times. piperita L.) was independently transformed with a homologous sense version of the 1-deoxy-b-xylulose-5-phosphate reductoisomerase cDNA and with a homologous antisense version of the menthofuran synthase cDNA, both driven by the CaMV 355 promoter. Two groups of transgenic ***plants*** were regenerated in the reductoisomerase expts., one of which remained normal in appearance and development; another was deficient in chlorophyll prodn. and grew slowly. Transgenic ***plants*** of normal appearance and growth habit expressed the reductoisomerase transgene strongly and constitutively, as detd. by RNA blot anal. and direct enzyme assay, and these ***plants*** accumulated substantially more essential oil (about 50% yield increase) without change in monoterpene compn. compared with wild-type. Chlorophyll-deficient ***plants*** did not afford detectable reductoisomerase mRNA or enzyme activity and yielded less essential oil than did wild-type ***plants*** , indicating cosuppression of the reductoisomerase ***gene*** . ***Plants*** transformed with the antisense version of the menthofuran synthase cDNA were normal in appearance but produced less than half of this undesirable monoterpene oil component than did wild-type mint grown under unstressed or ***stressed*** conditions. These expts. demonstrate that essential oil quantity and quality can be ***regulated*** by metabolic engineering. Thus, alteration of the committed step of the mevalonate-independent pathway for supply of terpenoid precursors improves flux through the pathway that leads to increased monoterpene prodn., and antisense manipulation of a ***selected*** downstream monoterpene biosynthetic step leads to improved oil compn.
RE.CNT 58 THERE ARE 58 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 15 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:540727 CAPLUS
DN 135:119556
TI Molecular breeding of environmental ***stress*** tolerant ***plants***
AU Kasuga, Mie; Yamaguchi-Shinozaki, Kazuko
CS Japan Int. Res. Cent. Agric. Sci., Tsukuba, 305-8686, Japan
SO Baiosaiensu to Indasutori (2001), 59(7), 445-450 CODEN: BIDSE6; ISSN: 0914-8981
PB Baioindasutori Kyokai
DT Journal; General Review
LA Japanese
AB A review with 13 refs., on mol. responses to cold, drought, or salinity ***stress*** , and approach to improve ***stress*** tolerance using mol. genetics, discussing isolation of drought ***stress*** tolerant ***genes*** including rd29A, transcription factors (DREB) ***regulating*** drought tolerant ***genes*** , ***stress*** responsiveness of transgenic ***plant*** with overexpressed DREB protein in Arabidopsis thaliana, and application of ***stress*** -responsive rd29A ***gene*** promoter.

L8 ANSWER 16 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:465510 CAPLUS
DN 135:192928
TI Networking senescence- ***regulating*** pathways by using Arabidopsis enhancer trap lines
AU He, Yuehui; Tang, Weining; Swain, Johnnie D.; Green, Anthony L.; Jack, Thomas P.; Gan, Susheng
CS Plant Physiology/Biochemistry/Molecular Biology Program, Department of Agronomy and Tobacco and Health Research Institute, University of Kentucky, Lexington, KY, 40546-0236, USA
SO Plant Physiology (2001), 126(2), 707-716 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
AB The last phase of leaf development, generally referred to as leaf senescence, is an integral part of ***plant*** development that involves massive programmed cell death. Due to a sharp decline of photosynthetic capacity in a leaf, senescence limits crop yield and forest ***plant*** biomass prodn. However, the biochem. components and ***regulatory*** mechanisms underlying leaf senescence are poorly characterized. Although several approaches such as differential cDNA screening, differential display, and cDNA subtraction have been employed to isolate senescence-assocd. ***genes*** (SAGs), only a limited no. of SAGs have been identified, and information regarding the ***regulation*** of these ***genes*** is fragmentary. Here we report on the utilization of enhancer trap approach toward the identification and anal. of SAGs. We have developed a sensitive large-scale screening method and have screened 1,300 Arabidopsis enhancer trap lines and have identified 147 lines in which the reporter ***gene*** GUS (.beta.-glucuronidase) is expressed in senescing leaves but not in non-senescing ones. We have systematically analyzed the ***regulation*** of .beta.-glucuronidase expression in 125 lines (genetically, each contains single T-DNA insertion) by six senescence-promoting factors, namely abscisic acid, ethylene, jasmonic acid, brassinosteroid, darkness, and dehydration. This anal. not only reveals the complexity of the ***regulatory*** circuitry but also allows us to postulate the existence of a network of senescence-promoting pathways. We have also cloned three SAGs from randomly ***selected*** enhancer trap lines, demonstrating that reporter expression pattern reflects the expression pattern of the endogenous ***gene*** .
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 17 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:371141 CAPLUS
DN 136:64998
TI Tobacco and Arabidiopsis SLT1 mediate salt tolerance of yeast
AU Matsumoto, Tracie K.; Pardo, Jose M.; Takeda, Satomi; Bressan, Ray A.; Hasegawa, Paul M.
CS Center for Plant Environmental Stress Physiology, Department of Horticulture and Landscape Architecture, Purdue University, West Lafayette, IN, 47907-1165, USA
SO Plant Molecular Biology (2001), 45(4), 489-500 CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer Academic Publishers

DT Journal
LA English
AB A tobacco cDNA (NtSLT1, for Nicotiana tabacum sodium- and lithium-tolerant) was isolated by functional complementation of the salt-sensitive phenotype of a calcineurin (CaN)-deficient yeast mutant (cnb.DELTA., ***regulatory*** subunit null). CaN is a Ca2+/calmodulin-dependent type 2B protein phosphatase that ***regulates*** Na+ homeostasis in yeast. This phosphatase modulates plasma membrane K+/Na+ ***selectivity*** through the activation of high-affinity K+ transport, and increases extracellular Na+ efflux by activation and transcriptional induction of the Na+/Li+ translocating P-type ATPase encoded by ENA1. Expression of N-terminally truncated NtSLT1 (Met-304), but not full-length protein, suppressed salt sensitivity of cnb1. Truncated NtSLT1 also increased salt tolerance of wild-type yeast, indicating functional sufficiency. NtSLT1 encodes a protein of yet unknown function but experimentation in yeast confirms it as a salt tolerance determinant. The Arabidopsis thaliana orthologue, AtSLT1, also suppressed salt sensitivity of cnb.DELTA. but only when expressed without the N-terminus (Met-301), suggesting that this region of the proteins from these evolutionarily diverse ***plant*** species contains an autoinhibitory domain. NtSLT1 enhanced transcription of the CaN-dependent ENA1 ***gene*** promoter and compensated the salt sensitivity of a mutant deficient in TCN1 - a transcription factor that is activated by CaN and then induces ENA1 expression. NtSLT1 partially suppressed the salt sensitivity of ena1-4 indicating that NtSLT1 has both ENA-dependent and independent functions. NtSLT1 suppressed spk1 hal4 (SPK1/HAL4 which encodes a serine-threonine kinase that ***regulates*** TRK1-2 transporters to have high K+/Na+ ***selectivity***) but not ena1-4 trk1-2 implicating the ENA-independent function to be through TRK1-2. Together, these results implicate SLT1 as a signal ***regulatory*** mol. that mediates salt tolerance by modulating Na+ homeostasis.
RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 18 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:328833 CAPLUS
DN 135:315944
TI ***Selection*** and identification of salt tolerant line of sainfoin from seed of first post-flight ***plant***
AU Xu, Yunyuan; Wang, Minggang; Jia, Jingfen
CS Institute of Botany, Chinese Academy of Sciences, Beijing, 100093, Peop. Rep. China
SO Shiyan Shengwu Xuebao (2001), 34(1), 11-15 CODEN: SYSWAE; ISSN: 0001-5334
PB Shanghai Kexue Jishu Chubanshe
DT Journal
LA Chinese
AB The ***selection*** and identification of salt tolerant line of sainfoin from the seeds of first post-flight ***plants*** were studied. The seeds of sainfoin (Onobrychis viciaefolia Scop.) were carried in the recoverable satellite 940703 and recovered from earth orbit from China in 1994. The progeny seeds were obtained by producing in field. The salt tolerant calluses were ***selected*** by screening seedling and callus on 1.5% NaCl-contg. medium, reviving growth on NaCl-free medium and ***selecting*** callus on 1.2% NaCl-contg. medium. The salt tolerant line callus maintained the normal ability to regenerate ***plant*** . The salt tolerant line callus exhibited cross-resistance to PEG ***stress*** . The variant appeared higher efficiency than control to accumulate proline under salt ***stress*** , however, under nonstress condition it had lower proline level than control, which suggested that the higher efficiency to synthesize proline under ***stress*** condition might be more important than higher level in tissue under nonstress condition. The mechanism of proline synthesis in the ***selected*** callus was considered to result from the alteration in ***gene*** sensitivity to water ***regulation*** at transcription level. Acrylamide gradient electrophoresis showed that new isoenzyme form with MW175kD and 75kD of superoxide dismutase and esterase resp. appeared in salt tolerant callus. It was indicated that the combination of space mutagenesis with tissue culture could be used for the ***selection*** of salt tolerant sainfoin line in vitro.

L8 ANSWER 19 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:168161 CAPLUS
DN 134:218000
TI Use of arabinogalactan protein fusion constructs in expressing proteins or peptides of pharmaceutical interest in transgenic ***plants***
IN Bailey, Andrea; Yu, Wenjin; Tuboly, Tamas; Nagy, Eva; Erickson, Larry
PA University of Guelph, Can.
SO PCT Int. Appl., 49 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 2001016339 A1 20010308 WO 2000-CA977 20000825
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRAI US 1999-151147P P 19990827
AB The invention provides a DNA mol. (construct) comprising a promoter region operatively assocd. with a arabinogalactan D-epitope fusion protein ***gene*** , which is operatively assocd. to a termination ***regulatory*** element. The invention relates that the arabinogalactan-D epitope fusion protein is composed of the first 237 amino acids of alfalfa arabinogalactan protein linked to a synthetic D-epitope of the S protein from porcine transmissible gastroenteritis virus (TGEV). The invention also relates that arabinogalactan protein can also be fused to a protein or peptide of pharmaceutical interest, which can be ***selected*** from a group consisting of an antibody, antigen (such as TGEV S protein), antibiotic, growth factor, hormone, lymphokine, activator, herbicide resistance enhancer, or ***stress*** resistance enhancer. The invention also provides a vector contg. said DNA mols. (constructs), and a ***plant*** cell transformed with said vector for the recombinant prodn. of fusion protein. The invention further provides for the use of the transformed ***plants*** for obtaining ***plant*** tissue which can be administered to animals. Finally, the invention provides the cDNA sequence encoding alfalfa arabinogalactan protein, and the sequences encoding the modified D-epitope of the S protein from TGEV. In the example section, the invention showed that mice immunized with exts. obtained from transgenic alfalfa or tobacco contg.

the arabinogalactan D-epitope fusion protein were able to produce anti-TGEV antibodies.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 20 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:131592 CAPLUS
DN 135:355354
TI Transgenic chicory (Cichorium intybus L.)
AU Abid, M.; Huss, B.; Rambour, S.
CS Laboratoire de Physiologie et Genetique Moleculaire Vegetales, Universite des Science et Techniques de Lille, Villeneuve d'Ascq, 59655, Fr.
SO Biotechnology in Agriculture and Forestry (2001), 47(Transgenic Crops II), 102-123 CODEN: BAFOEG; ISSN: 0934-943X
PB Springer-Verlag
DT Journal
LA English
AB The aim of the study was: (1) to compare the ability of genetic transformation of different organs by Agrobacterium tumefaciens strains contg. the neomycin phosphotransferase II ***gene*** as a ***selectable*** marker; (2) to analyze how uidA coding for P-glucuronidase and used as a reporter ***gene*** is controlled by either constitutive (35 S of Cauliflower Mosaic Virus) or inducible (mas2' of mannopine synthase) promoters; (3) to analyze how uidA is expressed in different organs at different developmental stages of R1-transformed chicory. Activation of mas2' and CaMV 35S promoters by wounding and by some growth ***regulators*** and the stability of the transgenes in R1 progeny were analyzed as well.
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 21 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:831874 CAPLUS
DN 135:41681
TI Isolation of 3 salt-induced low-abundance cDNAs from light-grown callus of Mesembryanthemum crystallinum by suppression subtractive hybridization
AU Yen, Hungchen Emilie; Wu, Su-Mei; Hung, Yu-Hui; Yen, Shi-Kae
CS Department of Botany, National Chung-Hsing University, Taichung, 40227, Taiwan
SO Physiologia Plantarum (2000), 110(3), 402-409 CODEN: PHPLAI; ISSN: 0031-9317
PB Munksgaard International Publishers Ltd.
DT Journal
LA English
AB A technique combining suppression polymerase chain reaction with suppression subtractive hybridization was used to clone low-abundance transcripts that showed enhanced expression during salt ***stress*** in light-grown callus of Mesembryanthemum crystallinum L., the ice ***plant*** . Three salt-induced cDNAs were ***selected*** by the prolonged film exposure time when analyzed by northern blotting. All of them showed different response kinetics to 200 mM NaCl, but were all expressed at increased levels in the presence of high salts at the cellular level. Anal. of nucleic acid and deduced amino acid sequences of these cDNAs revealed that they encoded a protein involved in K+ uptake (suppressor of K+ transport growth defect [SKD1]), an enzyme in the ubiquitin-mediated proteolytic cycle (ubiquitin-conjugating enzyme [UBC]; EC 6.3.2.19), and a low-mol. mass basic ***stress*** -induced protein. The SKD1-like ***gene*** was constitutively expressed in the root and up-***regulated*** in the leaf upon salt ***stress*** . The levels of other two transcripts remained relatively unchanged in the leaf and increased in the root by high salt. The possible roles of these ***gene*** products in the mechanism of salt tolerance in this halophyte are discussed.
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 22 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:806604 CAPLUS
DN 133:345580
TI Cloning and ***regulated*** expression of Aequorea victoria green fluorescent protein ***gene*** and uses thereof
IN Chalfie, Martin; Prasher, Douglas
PA The Trustees of Columbia University In the City of New York, USA; Woods Hole Oceanographic Institution
SO U.S., 13 pp., Cont.-in-part of U.S. Ser. No. 192,274, abandoned. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI US 6146826 A 20001114 US 1996-367236 19960618 US 5491084 A 19960213 US 1993-119678 19930910 WO 9507463 A1 19950316 WO 1994-US10165 19940909 W: AU, CA, JP, KR, US, US RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
PRAI US 1993-119678 A2 19930910 US 1994-192274 B2 19940204 WO 1994-US10165 W 19940909
AB This invention provides a cell comprising a DNA mol. having a ***regulatory*** element from a ***gene*** , other than a ***gene*** encoding a green fluorescent protein operatively linked to a DNA sequence encoding the green fluorescent protein. This invention also provides living organisms which comprise the above-described cell. This invention also provides : (a) introducing into the cells a DNAI mol. having DNA sequence encoding the protein of interest and DNAII mol. having DNA sequence encoding a green fluorescent protein; (b) culturing the introduced cells under conditions permitting expression of the green fluorescent protein and the protein of interest; and (c) ***selecting*** the cultured cells which express green fluorescent protein, thereby ***selecting*** cells expressing the protein of interest. Finally, this invention provides various uses of a Aequorea victoria green fluorescent protein.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 23 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:722042 CAPLUS
DN 134:3525
TI The human DIMINUTO/DWARF1 homolog seladin-1 confers resistance to Alzheimer's disease-associated neurodegeneration and oxidative ***stress***
AU Greeve, Isabell; Hermans-Borgmeyer, Irm; Brellinger, Claire; Kasper, Dagmar; Gomez-Isla, Teresa; Behl, Christian; Levkau, Bodo; Nitsch, Roger M.
CS Center for Molecular Neurobiology Hamburg, University of Hamburg, Hamburg, 20246, Germany
SO Journal of Neuroscience (2000), 20(19), 7345-7352 CODEN: JNRSDS; ISSN: 0270-6474
PB Society for Neuroscience

DT Journal
LA English
AB In Alzheimer's disease (AD) brains, ***selected*** populations of neurons degenerate heavily, whereas others are frequently spared from degeneration. To address the cellular basis for this ***selective*** vulnerability of neurons in distinct brain regions, the authors compared ***gene*** expression between the severely affected inferior temporal lobes and the mostly unaffected fronto-parietal cortices by using an mRNA differential display. The authors identified seladin-1, a novel ***gene*** , which was downregulated in large pyramidal neurons in vulnerable regions in AD but not control brains. Seladin-1 is a human homolog of the DIMINUTO/DWARF1 ***gene*** described in ***plants*** and Caenorhabditis elegans. Its sequence shares similarities with flavin-adenine-dinucleotide (FAD)-dependent oxidoreductases. In human control brain, seladin-1 was highly expressed in almost all neurons. In PC12 cell clones that were ***selected*** for resistance against AD-assocd. amyloid-.beta. peptide (A.beta.)-induced toxicity, both mRNA and protein levels of seladin-1 were approx. threefold higher as compared with the non-resistant wild-type cells. Functional expression of seladin-1 in human neuroglioma H4 cells resulted in the inhibition of caspase 3 activation after either A.beta.-mediated toxicity or oxidative ***stress*** and protected the cells from apoptotic cell death. In apoptotic cells, however, endogenous seladin-1 was cleaved to a 40 kDa deriv. in a caspase-dependent manner. These results establish that seladin-1 is an important factor for the protection of cells against A.beta. toxicity and oxidative ***stress*** , and they suggest that seladin-1 may be involved in the ***regulation*** of cell survival and death. Decreased expression of seladin-1 in specific neurons may be a cause for ***selective*** vulnerability in AD.
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 24 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:718252 CAPLUS
DN 133:264097
TI Transgenic ***plants*** expressing trehalose-6-phosphate synthase ***gene*** from ***regulated*** promoter
IN Londesborough, John; Tunnela, Outi; Holmstrom, Kjell-Ove; Mantyla, Einar; Welin, Bjorn; Mandal, Abul; Palva, Tapio E.
PA BTG International Ltd., UK
SO U.S., 21 pp., Cont.-in-part of U.S. 5,792,921. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 4 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI US 6130368 A 20001010 US 1997-765691 19970318 US 5422254 A 19950606 US 1992-841997 19920228 WO 9317093 A2 19930902 WO 1993-FI49 19930215 WO 9317093 A3 19930930 W: AT, AU, BB, BG, BR, CA, CH, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, LK, LU, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, SN, TD, TG US 5792921 A 19980811 US 1994-290301 19940815 WO 9600789 A1 19960111 WO 1995-FI377 19950629 W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TT RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG
PRAI US 1992-836021 B1 19920214 US 1992-841997 A2 19920228 WO 1993-FI49 A2 19930215 FI 1994-3133 A 19940629 US 1994-290301 A2 19940815 WO 1995-FI377 W 19950629
AB The present invention concerns transgenic ***plants*** producing trehalose and methods of increasing the trehalose content of ***plants*** . According to the invention, the ***plants*** of interest are transformed with the coding sequence of a ***gene*** for trehalose-6-phosphate synthase fused to a non-constitutive ***plant*** promoter, which allows for temporal, topol. or ***stress*** -induced control over the expression of the ***gene*** . The invention can be used for protecting staple crop ***plants*** against drought, high salinity or temp. extremes and for improving the storage properties of harvested ***plants*** including green food stuffs, picked fruits and ornamental ***plants*** . The TPS1 ***gene*** for the catalytic subunit of the yeast TPS under control of the Arabidopsis thaliana Rubisco small subunit ***gene*** promoter (Pats1A) was introduced into tobacco using kanamycin resistance as a ***selectable*** marker. Wenty of 26 transgenic ***plants*** produced material reacting with anti-TSP antibodies and had leaf trehalose levels 4-4--fold greater than those of control ***plants*** . Detached leaves of high-trehalose transformants showed greater resistance than to drying than those of control ***plants*** .
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 25 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:411007 CAPLUS
DN 133:132511
TI Enhancement of Na+ uptake currents, time-dependent inward-rectifying K+ channel currents, and K+ channel transcripts by K+ starvation in wheat root cells
AU Buschmann, Peter H.; Vaidyanathan, Rama; Gassmann, Walter; Schroeder, Julian I.
CS Department of Biology and Center for Molecular Genetics, University of California at San Diego, La Jolla, CA, 92093-0116, USA
SO Plant Physiology (2000), 122(4), 1387-1397 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
AB The effects of K+ starvation on Na+ and K+ uptake mechanisms in the plasma membrane of wheat (Triticum aestivum L.) root cortex cells were studied using the patch-clamp technique. Unexpectedly, K+ starvation of wheat seedlings was found to enhance the magnitude and frequency of occurrence of time-dependent inward-rectifying K+ channel currents (IK+in). The author examd. whether the transcription of a wheat root K+in channel ***gene*** is induced by K+ starvation. A cDNA coding for a wheat root K+ channel homolog, TaAKT1 (accession no. AF207745), was isolated. TaAKT1 mRNA levels were up- ***regulated*** in roots in response to withdrawal of K+ from the growth medium. Furthermore, K+ starvation caused an enhancement of instantaneous Na+ currents (INa+). Electrophysiol. analyses suggested that IK+in and INa+ are not mediated by the same transport protein based on: (a) different activation curves, (b) different time dependencies, (c) different sensitivities to external Ca2+, and (d) different cation ***selectivities*** . These data implicate a role for INa+ in Na+ uptake and

stress during K+ starvation, and indicate that K+in channels may contribute to K+-starvation-induced K+ uptake in wheat roots.
RE.CNT 74 THERE ARE 74 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 26 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:325844 CAPLUS
DN 133:247986
TI A xenobiotic- ***stress*** -activated transcription factor and its cognate target ***genes*** are preferentially expressed in root tip meristems
AU Klinedinst, Susan; Pascuzzi, Pete; Redman, Julia; Desai, Mihir; Arias, Jonathan
CS Center for Agricultural Biotechnology, University of Maryland Biotechnology Institute and Dept. of Chemistry and Biochemistry, University of Maryland, College Park, MD, 20742, USA
SO Plant Molecular Biology (2000), 42(5), 679-688 CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer Academic Publishers
DT Journal
LA English
AB In ***plants*** , as-1-type cis elements and their trans-acting factors confer tissue-specific and signal-responsive activities to the promoters of several glutathione S-transferase (GST) ***genes*** . ***Regulation*** of as-1 is widely thought to involve trans-acting factors that belong to a family of basic/leucine-zipper "TGA factors" that ***selectively*** bind this element. The authors have previously shown that TGA1a, a highly conserved TGA factor of tobacco, enhances transcription through as-1 in response to xenobiotic-***stress*** cues. To better understand the functional contribution of this transcription factor to the expression of as-1- ***regulated*** ***genes*** , the authors have studied its tissue- and cell-specific localization in tobacco seedlings. The authors show here that the relative amt. of TGA1a transcripts expressed in roots and shoots correlate with the as-1- ***regulated*** , basal-level expression of a GUS transgene and two putative target GST ***genes*** . In situ hybridization of intact seedlings demonstrated that TGA1a and these GST ***genes*** are preferentially expressed in root tip meristems. Similar findings were made with a ***gene*** -specific probe for PG13, a homolog of TGA1a, demonstrating that both factors are likely to be present in the same root meristem cells. Furthermore, TGA1a protein was immunol. detected exclusively in the primary root and its meristem. Collectively, these studies suggest that TGA1a, and perhaps PG13, may contribute to the expression of GST isoenzymes, esp. in root tip meristems. The biol. significance of these observations is discussed.
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 27 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:283139 CAPLUS
DN 133:276984
TI The isolation of ***genes*** from the resurrection grass Sporobolus stapfianus which are induced during severe drought ***stress***
AU Neale, A. D.; Blomstedt, C. K.; Bronson, P.; Le, T. -N.; Guthridge, K.; Evans, J.; Gaff, D. F.; Hamill, J. D.
CS Department of Biological Sciences, Monash University, Melbourne, 3168, Australia
SO Plant, Cell and Environment (2000), 23(3), 265-277
CODEN: PLCEDV; ISSN: 0140-7791
PB Blackwell Science Ltd.
DT Journal
LA English
AB A modification of the "cold plaque" screening technique was used to screen a cDNA library constructed from drought-***stressed*** leaf tissue of the desiccation tolerant ("resurrection") grass Sporobolus stapfianus. This technique allowed a large no. of clones representing ***genes*** expressed at low abundance to be isolated. An examn. of expression profiles revealed that several of these ***genes*** are induced in desiccation-tolerant tissue experiencing severe drought ***stress*** . Further characterization indicated that the ***gene*** products encoded include an eIF1 protein translation initiation factor and a glycine- and proline-rich protein which have not previously been assocd. with drought ***stress*** . In addn., ***genes*** encoding a serine/threonine phosphatase type 2C, a tonoplast-intrinsic protein (TIP) and an early light-inducible protein (ELIP) were isolated. A no. of these ***genes*** are expressed differentially in desiccation-tolerant and desiccation-sensitive tissues, suggesting that they may be assocd. with the desiccation tolerance response of S. stapfianus. The results indicate that there may be unique ***gene*** ***regulation*** processes occurring during induction of desiccation tolerance in resurrection ***plants*** which allow different drought-responsive ***genes*** to be ***selectively*** expressed at successive levels of water loss.
RE.CNT 71 THERE ARE 71 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 28 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:255499 CAPLUS
DN 133:27235
TI Improved biomass productivity and water use efficiency under water deficit conditions in transgenic wheat constitutively expressing the barley HVA1 ***gene***
AU Sivamani, E.; Bahieldin, A.; Wraith, J. M.; Al-Niemi, T.; Dyer, W. E.; Ho, T.-H. D.; Qu, R.
CS Department of Plant Sciences, Montana State University, Bozeman, MT, USA
SO Plant Science (Shannon, Ireland) (2000), 155(1), 1-9
CODEN: PLSCE4; ISSN: 0168-9452
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB The ABA-responsive barley ***gene*** HVA1, a member of group 3 late embryogenesis abundant (LEA) protein ***genes*** , was introduced into spring wheat (Triticum aestivum L.) cv. Hi-Line using the biolistic bombardment method. High levels of expression of the HVA1 ***gene*** , ***regulated*** by the maize ubi1 promoter, were obsd. in leaves and roots of independent transgenic wheat ***plants*** and were inherited by offspring generations. T3 progenies of four ***selected*** transgenic wheat lines were tested under greenhouse conditions for tolerance of soil water deficit. Potted ***plants*** were grown under moderate water deficit and well-watered conditions, resp. Two homozygous and one heterozygous transgenic lines expressing the HVA1 ***gene*** had significantly ($P<0.01$) higher water use efficiency values, 0.66-0.68 g kg-1, as compared to 0.57 and 0.53 g kg-1, resp., for the nonexpressing transgenic and nontransgenic controls under moderate water deficit conditions. The two homozygous transgenic ***plant*** lines also had significantly greater

total dry mass, root fresh and dry wts., and shoot dry wt. compared to the two controls under soil water deficit conditions. Results of this study indicate that growth characteristics were improved in transgenic wheat ***plants*** constitutively expressing the barley HVA1 ***gene*** in response to soil water deficit.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 29 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:241827 CAPLUS
DN 133:2494
TI Lignins and lignification: ***selected*** issues
AU Boudet, Alain-M.
CS Pole de biotechnologie vegetale, UMR CNRS/UPS 5546, Castanet-Tolosan, 31326, Fr.
SO Plant Physiology and Biochemistry (Paris) (2000), 38(1/2), 81-96 CODEN: PPBIEX; ISSN: 0981-9428
PB Editions Scientifiques et Medicales Elsevier
DT Journal; General Review
LA English
AB A review with 78 refs. Lignin deposition in ***plant*** cell walls is one of the mechanisms which allowed the development of upright ***plants*** adapted to a terrestrial habitat. At the present time, lignins and lignification are the subject of very active research which has recently moved from chem. and biochem. aspects to more biol. and developmental problems. In this review, three different topics will be addressed. (a) A first section will deal with recent advances related to the biosynthesis of lignins. It will be shown that a complex array of O-methyltransferases may control the prodn. of differentially methylated monolignols, the precursors of lignins, but that the downstream enzymes in the synthesis of monolignols are probably not encoded by multigene families which would provide addnl. possibilities for fine-tuning the monomeric compn. of lignins. In addn., recent results obtained on laccases will illustrate the difficulty in identifying the true nature of oxidases involved in the prodn. of phenoxy radicals, the oxidn. products of monolignols. (b) A second set of data will highlight the potential interest of Arabidopsis mutants for understanding lignin synthesis, deposition and function. Indeed, different classes of lignification mutants with modifications in lignin content or compn. and alterations of vascular differentiation or global vascular pattern have already been characterized. The identification of the corresponding ***genes*** will undoubtedly give rise to new insights on key steps and ***regulation*** mechanisms in the lignification process. (c) The last section is dedicated to the future of lignin genetic engineering. It will be emphasized that, after a first period which has demonstrated the potential of the approach, it is necessary to consider in greater detail the unexpected side effects and compensation mechanisms assocd. with induced lignin modifications. New targets for future lignin genetic engineering expts. will be identified and the extension of the technol. to new woody species, the advantages for the pulp industry and the problems assocd. with public perception of these new products will be envisaged. Lignification is a tightly ***regulated*** and dynamic process subject to modulation at different levels during normal development and in response to different ***stresses*** . Understanding these subtle mechanisms which also involve the other polymers of the cell wall is an important challenge facing ***plant*** biol. as we enter the next century.
RE.CNT 78 THERE ARE 78 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 30 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:81175 CAPLUS
DN 132:261277
TI ABFs, a family of ABA-responsive element binding factors
AU Choi, Hyung-In; Hong, Jung-Hee; Ha, Jin-Ok; Kang, Jung-Youn; Kim, Soo Young
CS Kumho Life and Environmental Science Laboratory, Kwangju, 500-712, S. Korea
SO Journal of Biological Chemistry (2000), 275(3), 1723-1730 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Abscisic acid (ABA) plays an important role in environmental ***stress*** responses of higher ***plants*** during vegetative growth. One of the ABA-mediated responses is the induced expression of a large no. of ***genes*** , which is mediated by cis- ***regulatory*** elements known as abscisic acid-responsive elements (ABREs). Although a no. of ABRE binding transcription factors have been known, they are not specifically from vegetative tissues under induced conditions. Considering the tissue specificity of ABA signaling pathways, factors mediating ABA-dependent ***stress*** responses during vegetative growth phase may thus have been unidentified so far. Here, we report a family of ABRE binding factors isolated from young Arabidopsis ***plants*** under ***stress*** conditions. The factors, isolated by a yeast one-hybrid system using a prototypical ABRE and named as ABFs (ABRE binding factors) belong to a distinct subfamily of bZIP proteins. Binding site ***selection*** assay performed with one ABF showed that its preferred binding site is the strong ABRE, CACGTGGC. ABFs can transactivate an ABRE-contg. reporter ***gene*** in yeast. Expression of ABFs is induced by ABA and various ***stress*** treatments, whereas their induction patterns are different from one another. Thus, a new family of ABRE binding factors indeed exists that have the potential to activate a large no. of ABA/***stress*** -responsive ***genes*** in Arabidopsis.
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 31 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:708882 CAPLUS
DN 131:333036
TI Arabidopsis thaliana ***gene*** ABI4, its DNA sequence and use in production of transgenic ***plants*** with enhanced ***stress*** -tolerance and extended seed storage stability
PA The Regents of the University of California, USA; The General Hospital Corporation
SO PCT Int. Appl., 68 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 9955840 A1 19991104 WO 1999-US8954 19990427 W: CA, JP RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE US 6248937 B1 20010619 US 1999-300672 19990427
PRAI US 1998-83334P P 19980427
AB The invention provides the DNA sequence of Arabidopsis thaliana ***gene*** ABI4 (abscisic acid (ABA)-insensitive 4),

as well as the corresponding amino acid sequence of the transcription factor encoded by the ABI4 ***gene*** . The DNA sequence of A. thaliana ***gene*** ABI4 is deposited at GenBank under Accession no. AF040959. The invention also provides the DNA sequence of the A. thaliana abi4 mutant allele, which results from a single base pair deletion. The invention further provides a method for modification and enhancement of seed or ***plant*** ***stress*** -tolerance which involves: (a) constructing an ABI4 transgene by fusing ABI4 coding sequence to a ***regulatory*** sequence (such as a promoter or cis- ***regulatory*** enhancer element) for overexpression; (b) transferring the ABI4 transgene into a recipient ***plant*** by Agrobacterium-mediated transformation, biolistic transformation or electroporation and (c) ***selecting*** homozygous transgenic ***plants*** from primary transformant lines by scoring a resistance to antibiotics or herbicides. The method for prodn. of transgenic ***plants*** results in recombinant prodn. of ***gene*** ABI4 transcription factor which results in enhanced survival properties for the transgenic ***plant*** , such as resistance to drought, salt or cold ***stresses*** and extended storage stability of seeds. The ABI4 was mapped to chromosome 2 using a single bacterial artificial chromosome (BAC) clone (TAMU7M7).
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 32 OF 32 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:194162 CAPLUS
DN 130:219173
TI Mammalian circadian rhythm-like ***gene*** sequence and therapeutic applications
IN Lee, Cheng-chi; Albrecht, Urs; Sun, Zhong Sheng; Eichele, Gregor
PA Research Development Foundation, USA
SO PCT Int. Appl., 74 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 9912952 A1 19990318 WO 1998-US18755 19980909
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG ZA 9808209 A 20000322 ZA 1998-8209 19980908 AU 9893808 A1 19990329 AU 1998-93808 19980909 US 6190882 B1 20010220 US 1998-150460 19980909
PRAI US 1997-58256P P 19970909 US 1997-65957P P 19971104 WO 1998-US18755 W 19980909
AB The present invention provides DNA encoding a RIGUI protein ***selected*** from the group consisting of: (a) isolated DNA which encodes a RIGUI protein; (b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a RIGUI protein; and (c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a RIGUI protein. Also provided is a vector capable of expressing the DNA adapted for expression in a recombinant cell and ***regulatory*** elements necessary for expression of the DNA in the cell. Further, a host cell transfected with the vector disclosed herein the vector expressing a RIGUI protein.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

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